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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:21:26 ; Search time 82 Seconds

(without alignments)
30.875 Million cell updates/sec

Title: US-09-781-796b-7

Sequence: 1 KSDPTETGALDLCGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	20	17	AAW04339
2	82	85.4	16	17	AAW04340
3	75	78.1	439	22	AAW1918
4	75	78.1	454	21	AAW10890
5	75	78.1	454	21	AAW10913
6	75	78.1	463	21	AAW10902
7	75	78.1	463	21	AAW10925
8	75	78.1	464	21	AAW10899
9	75	78.1	464	21	AAW10922
10	75	78.1	473	21	AAW10901

ALIGNMENTS

RESULT 1
ID AAW04339 standard; Protein: 20 AA.

AC AAW04339;

DT 29-DEC-1996 (first entry)

XX ATP diphosphohydrolase fragment from pig pancreas.

XX ATP diphosphohydrolase; Appase; bovine aorta; pig pancreas;

KW apyrase; CD39; lymphoid cell activation antigen; enzyme;

KM platelet aggregation; thrombogenicity; anti-haemostatic.

XX OS Sus. scrofa.

PN W09632471-A2

PD 17-OCT-1996.

PF 10-APR-1996; 96MO-CA00223.

PR 10-APR-1995; 95US-0419204.

PA (UYSH) UNITV SHERBROOKE.

PI Beaudoin AR, Sevigny J;

DR WPI; 1996-477122/47.

XX Isolated ATP diphosphohydrolase enzymes - have anti-haemostatic

PT activity, useful for reducing platelet aggregation and

PT thrombogenicity

11 75 78.1 473 21 AAW0924
12 75 78.1 474 21 AAW0990
13 75 78.1 474 21 AAW0923
14 75 78.1 476 21 AAW0888
15 75 78.1 476 21 AAW0889
16 75 78.1 476 21 AAW0891
17 75 78.1 476 21 AAW0912
18 75 78.1 478 21 AAW0891
19 75 78.1 478 21 AAW0914
20 75 78.1 487 21 AAW0898
21 75 78.1 487 21 AAW0921
22 75 78.1 510 17 AAW04334
23 75 78.1 510 17 AAW04334
24 75 78.1 510 21 AAW0887
25 75 78.1 510 21 AAW0910
26 75 78.1 510 22 AAW1917
27 75 78.1 405 21 AAW44851
28 64 66.7 405 22 AAW72239
29 64 66.7 405 22 AAW44850
30 64 66.7 428 21 AAW44850
31 64 66.7 428 22 AAW72238
32 64 66.7 428 22 AAW72240
33 64 66.7 428 22 AAW72243
34 64 66.7 428 22 AAW19883
35 64 66.7 465 23 AAE19884
36 64 66.7 529 23 AAW6973
37 62 64.6 529 23 AAW6973
38 60 62.5 330 21 AAW53336
39 52 54.2 458 22 AAW33296
40 52 54.2 495 20 AAW30882
41 49 51.0 462 20 AAW85684
42 48 50.0 462 23 AAW78818
43 46.5 48.4 604 23 AAE18106
44 46 47.9 456 22 AAW93929
45 46

Human soluble CD39
Protein encoded by
Human soluble CD39
Protein encoded by
Protein encoded by
Human CD39-L4-1 pr
Human CD39-L4-2/3
Protein encoded by
Human soluble CD39
Protein encoded by
Human soluble CD39
Human lymphoid cel
Human soluble CD39
Human soluble CD39
Human CD39-L66 pro
Human CD39-L66 pr
Human CD39-L4 prot
Human CD39-L4 var1
Human CD39-Like pr
Human CD39-Like pr
Human CD39-L4 prote
Mouse CD39-L4 prote
Human CD39-L4 prote
Human CD39-Like ge
Human colon cancer
Human PRO polypept
Human membrane spa
Novel human secret
NP46 root lectin.
Dolichos biflorus
Human nucleoside p
Human polypeptide,

XX Claim 3; Page 46; 60pp; English.

PS The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
 XX pancreatic (AAW04339) ATPases have been partially sequenced.
 CC The sequences have been found to be highly homologous to a human
 CC lymphoid cell activation antigen designated CD39 (Maliszewski et
 CC al. (1994). J. Immunol.: 3574-3583). The complete sequences of the
 CC ATPases types I and II have not been obtained yet. Assuming that
 CC the CD39 gene product is an ATPase type II, the use of CD39
 CC in the reduction of platelet aggregation and of thrombogenicity
 CC may be contemplated, as well as a process of making ATPases
 CC using the CD39 sequence (AAT38516).

XX Sequence 20 AA;

Query Match 100.0%; Score 96; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5,8e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSDQETFGALDVGASTQ 19
 |||||
 Db 1 KSDQETFGALDVGASTQ 19

RESULT 2

AAW04340
 ID AAW04340 standard; Protein; 16 AA.

AC AAW04340;

DT 29-DEC-1996 (first entry)

XX ATP diphosphohydrolase fragment (5) from bovine aorta.

XX ATP diphosphohydrolase; ATPase; bovine aorta; pig pancreas;
 KW apyrase; CD39; lymphoid cell activation antigen; enzyme;
 KW platelet aggregation; thrombogenicity; anti-haemostatic.

OS Bos taurus.

XX W09632471-A2.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-CA00223.

XX 10-APR-1995; 95US-0419204.

XX (UYSH) UNIV SHERBROOKE.

XX Beaudoin AR, Sevigny J;

XX WPI; 1996-477122/47.

XX Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic
 PT activity, useful for reducing platelet aggregation and
 PT thrombogenicity

XX Claim 2; Page 47; 60pp; English.

CC The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
 CC pancreatic (AAW04339) ATPases have been partially sequenced.
 CC The sequences have been found to be highly homologous to a human
 CC lymphoid cell activation antigen designated CD39 (Maliszewski et
 CC al. (1994). J. Immunol.: 3574-3583). The complete sequences of the
 CC ATPases types I and II have not been obtained yet. Assuming that
 CC the CD39 gene product is an ATPase type II, the use of CD39
 CC in the reduction of platelet aggregation and of thrombogenicity
 CC may be contemplated, as well as a process of making ATPases
 CC using the CD39 sequence (AAT38516).

XX Sequence 16 AA;

Query Match 85.4%; Score 82; DB 17; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSDQETFGALDVGGA 16
 |||||
 Db 1 KSDQETFGALDVGGA 16

RESULT 3

AAW71918
 ID AAW71918 standard; Protein; 439 AA.

AC AAW71918;

DT 09-MAY-2001 (first entry)

XX Soluble human CD39 polypeptide.

XX Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
 KW stroke; thrombotic disorder; ischaemic disorder.

OS Homo sapiens.

XX W020011949-A1.

XX 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US22060.

XX 13-AUG-1999; 99US-0374586.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Pinsky DJ;

XX WPI; 2001-202805/20.

XX Treating stroke in a subject susceptible to intracranial hemorrhaging
 PT and an ischemic disorder, involves administering a CD39 polypeptide
 PT which inhibits ADP-mediated platelet aggregation or leukocyte
 PT accumulation

XX Claim 3; Page 14; 118pp; English.

XX The present sequence is the active fragment of human CD39. CD39 or its
 CC active fragment may be administered to treat or prevent stroke in a
 CC subject susceptible to intracranial haemorrhaging or an ischaemic
 CC disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
 CC or leukocyte accumulation and/or ADP by increasing ADP catabolism to the
 CC subject. CD39 or its active fragment is useful for treating or preventing
 CC stroke, thrombotic disorders and ischaemic disorders such as peripheral
 CC vascular disorder, pulmonary embolus, venous thrombosis, myocardial
 CC infarction, transient ischaemic attack, unstable angina, reversible
 CC ischaemic neurological deficit and sickle cell anaemia. It is also
 CC useful for treating or preventing a stroke disorder in a subject
 CC undergoing heart surgery, lung surgery, spinal surgery, brain surgery,
 CC vascular surgery, abdominal surgery, or organ transplantation surgery.

XX Sequence 439 AA;

Query Match 78.1%; Score 75; DB 22; Length 439;
 Best Local Similarity 73.7%; Pred. No. 0.00011;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETFGALDVGASTQ 19
 ::::|
 Db 165 ETNNQETFGALDVGASTQ 183

RESULT 4

AAV70890

ID AAY70890 standard; Protein: 454 AA.

XX AAY70890;

XX 17-AUG-2000 (first entry)

XX Protein encoded by fusion construct of human soluble CD39 cDNA-1.

DE Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 XX unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiatic;
 KW cerebroprotective; antiatherosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Protein 1..15

FT /label= Mature_human_interleukin_2
 FT /note= "N-terminal region"
 FT Protein 16..454
 FT /note= "Human soluble CD39 protein"

XX WO200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US23641.

XX 16-OCT-1998; 98US-0104585.

XX 06-NOV-1998; 98US-0107466.

XX 13-AUG-1999; 99US-0149010.

XX (IMMV) IMMUNEX CORP.

XX (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

XX N-PSDB; AAD00201.

XX Inhibiting platelet activation and recruitment, useful for treating a

XX mammal suffering from unstable angina, myocardial infarction, stroke,

XX coronary artery disease or injury, comprises administering soluble CD39

XX polypeptides -

XX Claim 6; Page 95-97; 118pp; English.

XX The present sequence is the protein encoded by a fusion construct of
 CC sol(soluble)CD39, having apyrase activity. Fusion of 12 amino acids from
 CC the N-terminus of mature human IL2 to the solCD39 coding region results
 CC in high levels of both expression and activity in the supernatants of
 CC transfected cells. This is used in the treatment of unstable angina,
 CC myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, coronary
 CC platelet-associated ischaemic disorder including lung ischaemia, embolism,
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.

XX Sequence 454 AA:

Query Match 78.1%; Score 75; DB 21; Length 454;

Best Local Similarity 73.7%; Pred. No. 0.00011;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDPQETGALDGGASTQ 19
 DB 180 ETNNQETFGALDGGASTQ 198

RESULT 5

AAV70913 standard; Protein: 454 AA.

XX AAV70913;

XX 17-AUG-2000 (first entry)

XX Human soluble CD39 and IL2 N-terminus comprising fusion construct.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;

XX unstable angina; myocardial infarction; stroke; coronary artery disease;

XX atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;

XX platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;

XX coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

XX thrombus formation; occlusion; stenosis; restenosis; antilanginal;

XX cardiatic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Protein 1..15

XX /label= Mature_human_interleukin_2

XX /note= "N-terminal region"

XX Protein 16..454

XX /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US22955.

XX 16-OCT-1998; 98US-0104585.

XX 06-NOV-1998; 98US-0107466.

XX 13-AUG-1999; 99US-0149010.

XX (IMMV) IMMUNEX CORP.

XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

XX N-PSDB; AAD00206.

XX New soluble CD39 polypeptides having apyrase activity, useful for

XX inhibiting angiogenesis and treating unstable angina, myocardial

XX infarction, stroke, coronary artery disease or injury -

XX Claim 6a; Page 95-97; 122pp; English.

XX The present sequence is a fusion construct, comprising the N-terminal
 CC amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
 CC region, that has apyrase activity. This results in high levels of
 CC solCD39 expression and activity in the transfected cells. Soluble CD39 is
 CC constructed by removing the N- and C-terminal transmembrane domains. It
 CC retains the capacity to metabolise ADP and ADP at relevant concentrations
 CC and the ability to block and reverse ADP-induced platelet activation and
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC are useful for inhibiting platelet activation, stroke, coronary artery
 CC disease or injury, atherosclerosis, peripheral vascular occlusion,
 CC preclampsia, embolism, platelet-associated ischaemic disorders including

CC lung, coronary and cerebral ischaemia, thrombotic disorders including
 CC coronary, peripheral and cerebral artery thrombosis, intracardiac and
 CC venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also
 CC useful for preventing thrombus formation or reformation, occlusion,
 CC reocclusion, stenosis or restenosis of blood vessels or stroke.
 XX

SO Sequence 454 AA;

Query Match 78.1%; Score 75; DB 21; Length 454;
 Best Local Similarity 73.7%; Pred. No. 0.00011;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDPTETGALDGGASTQ 19
 Db 180 ETNNDETFGALDGGASTQ 198

RESULT 6
 AAY70902

ID AAY70902 standard; Protein: 463 AA.

AC AAY70902;

DT 17-AUG-2000 (first entry)

DE Protein encoded by I9kappalsolCD39 construct.

XX Soluble CD39: ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; transient ischaemic attack; thrombus formation;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antilanginal; carotid;
 KW cerebroprotective; antilarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion; I9kappalsolCD39 construct.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 XX Peptide 1..20
 XX Cleavage-site /note= "I9kappa leader sequence"
 XX Region 20..21
 XX Region 21..24
 XX Region /note= "Derived from IL-2"
 XX Region 25..32
 XX Region /note= "Derived from solCD39"
 XX Region 25..463
 XX /note= "Soluble portion of CD39"

WO200023094-A2.

PD 27-APR-2000.

PF 13-OCT-1999; 99WO-US23641.

PR 16-OCT-1998; 98US-0104585.

PR 06-NOV-1998; 98US-0107466.

PR 13-AUG-1999; 99US-0149010.

PA (IMMUNEX CORP.

PA (CORR) CORNELL RES FOUND INC.

PI Maliszewski CR, Gayle RB, Marcus AJ;

PD WPI; 2000-339518/29.

PT Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,

PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 XX
 XX Claim 6: Page 116-118; 118pp; English.

CC The present sequence is the protein encoded by I9kappalsolCD39 construct.
 CC This is used for transient expression of soluble(sol)CD39 in recombinant
 CC cells for determining enzymatic activity and platelet inhibitory activity
 CC for each protein product. solCD39 is used in the treatment of unstable
 CC angina, myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC peripheral artery thrombosis, venous thrombosis, intracardiac thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.
 XX

SO Sequence 463 AA;

Query Match 78.1%; Score 75; DB 21; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDPTETGALDGGASTQ 19
 Db 189 ETNNDETFGALDGGASTQ 207

RESULT 7
 AAY70925

ID AAY70925 standard; Protein: 463 AA.

AC AAY70925;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 fusion protein construct, I9kappalsolCD39.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antilanginal; cerebroprotective; antilarteriosclerotic; anticoagulant;
 KW carotid; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig;
 KW immunoglobulin kappa.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= "Leader-peptide"
 XX /note= "Derived from human immunoglobulin Ig kappa"
 XX Cleavage-site 20..21
 XX Region 21..24
 XX Region /note= "Cleavage site of leader sequence"
 XX Protein 25..463
 XX /note= "Residues derived from human interleukin 2 (IL2)"
 XX /note= "Human soluble CD39 protein"

WO200023459-A1.

PD 27-APR-2000.

PF 13-OCT-1999; 99WO-US22955.

PR 16-OCT-1998; 98US-0104585.
 PR 06-NOV-1998; 98US-0107466.

PR 13-AUG-1999; 99US-0149010.
 XX (IMMUNEX CORP.
 PA Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX WPI: 2000-339644/29.
 DR
 XX New soluble CD39 polypeptides having apyrase activity, useful for
 PT inhibiting angiogenesis and treating unstable angina, myocardial
 PT infection, stroke, coronary artery disease or injury -
 XX
 PS Claim 6: Page 116-118; 122pp: English.
 XX
 XX The present sequence is the fusion protein construct, 19kappaSolCD39,
 CC This construct comprises of the leader peptide from human Immunoglobulin
 CC Ig kappa, linked to the soluble CD39 (solCD39) protein region by few
 CC residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase
 CC activity and is constructed by removing the N- and C-terminal
 CC transmembrane domains. It retains the capacity to metabolize ATP and ADP
 CC at relevant concentrations and the ability to block and reverse
 CC ADP-induced platelet activation and recruitment, including platelet
 CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
 CC angiologenesis. It is useful for the treatment of unstable angina, stroke,
 CC myocardial infarction, coronary artery disease or injury, embolism,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
 CC associated ischemic disorders including lung, coronary and cerebral
 CC ischemia, thrombotic disorders including coronary, peripheral and
 CC cerebral artery thrombosis, intracardiac and venous thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
 CC transient ischemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC stenosis of blood vessels or stroke.
 CC
 XX
 SQ Sequence 463 AA:
 Query Match 78.1%; Score 75; DB 21; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSDPTETFGALDGGASTQ 19
 DB 189 ETNNGETFGALDGGASTQ 207
 ID AAT70899 standard; Protein: 464 AA.
 AC AAT70899;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by Trm1 construct.
 XX
 XX Soluble CD39: ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischemic disorder; lung ischemia; thrombolytic;
 KW cerebral ischemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiant;
 KW cerebroprotective; antiatherosclerotic; vasotropic; anticoagulant;
 KW coronary ischemia; vascular occlusion; pIL2Trm1 variant.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 24..25
 FT Protein 26..464

note="Soluble portion of CD39"

FT
 XX WO200023094-A2.
 PN
 XX 27-APR-2000.
 PD
 XX 13-OCT-1999; 99WO-US23641.
 PE
 XX 16-OCT-1998; 98US-0104585.
 PR 06-NOV-1998; 98US-0107466.
 PR 13-AUG-1999; 99US-0149010.
 XX
 XX (IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 PI WPI: 2000-339518/29.
 DR
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 XX
 PS Example 11: Page 111-112; 118pp: English.
 XX
 XX The present sequence is the protein encoded by Trm1 construct, pIL2Trm1
 CC variant was constructed by removing the human IL2 residues from solCD39
 CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
 CC human IL2 to the solCD39 coding region results in high levels of both
 CC expression and activity in the supernatants of transfected cells. SolCD39
 CC is used in the treatment of unstable angina, myocardial infarction,
 CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
 CC vascular occlusion, preclampsia, embolism, platelet-associated ischemic
 CC disorder including lung ischemia, coronary ischemia and cerebral
 CC ischemia, a thrombotic disorder including coronary artery thrombosis,
 CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 CC thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack.
 CC Soluble CD39 is also useful for preventing thrombus formation or
 CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
 CC vessels or stroke.
 CC
 XX
 SQ Sequence 464 AA:
 Query Match 78.1%; Score 75; DB 21; Length 464;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSDPTETFGALDGGASTQ 19
 DB 190 ETNNGETFGALDGGASTQ 208
 ID AAT70922 standard; Protein: 464 AA.
 AC AAT70922;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Human soluble CD39 fusion protein construct, pIL2Trm1.
 XX
 XX Soluble CD39: solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antilanginal; cerebroprotective; antiatherosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
 KW

AA	RESULT 11
XX	AAV70924
AC	AAV70924 standard; Protein; 473 AA.
XX	AAV70924;
XX	17-ANG-2000 (first entry)
DE	Human soluble CD39 fusion protein construct, pIL2Trimm4.
XX	Soluble CD39; solCD39; human; apyrase activity; platelet activation;
XX	unstable angina; myocardial infarction; stroke; coronary artery disease;
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW	platelet-associated ischemic disorder; thrombotic disorder; reocclusion;
KW	coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW	thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KM	antithrombotic; cerebroprotective; antithrombotic; anticoagulant;
KM	cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
OS	Homo sapiens.
OS	Synthetic.
XX	Key
XX	Location/Qualifiers
XX	Peptide
FT	1..24
FT	/label="Leader peptide
FT	/note="Derived from human interleukin 2 (hIL2)"
FT	Cleavage-site
FT	26..27
FT	/note="Cleavage site of leader sequence"
FT	35..473
FT	/note="Human soluble CD39 protein"
XX	MO200023459-A1.
XX	27-APR-2000.
XX	13-OCT-1999; 99WO-US22955.
XX	16-OCT-1998; 98US-010455.
PR	06-NOV-1998; 98US-0107466.
PR	13-AUG-1999; 99US-0149010.
XX	(IMVX) IMMUNEX CORP.
XX	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
DR	WPI; 2000-339644/29.
XX	New soluble CD39 polypeptides having apyrase activity, useful for
PT	inhibiting angiogenesis and treating unstable angina, myocardial
PT	infarction, stroke, coronary artery disease or injury -
XX	Claim 6; Page 114-116; 122pp; English.
XX	The present sequence is the fusion protein construct, pIL2Trimm4. This
CC	construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC	and soluble CD39 (solCD39) protein region, having apyrase activity.
CC	Soluble CD39 is constructed by removing the N- and C-terminal
CC	transmembrane domains. It retains the capacity to metabolize ATP and ADP
CC	at relevant concentrations and the ability to block and reverse
CC	ADP-induced platelet activation and recruitment, including platelet
CC	aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC	aggregation. It is useful for the treatment of unstable angina, stroke,
CC	myocardial infarction, coronary artery disease or injury, embolism,
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
CC	associated ischemic disorders including lung, coronary and cerebral
CC	ischemia, thrombotic disorders including coronary, peripheral and
CC	cerebral artery thrombosis, intracardiac and venous thrombosis,
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC	transient ischemic attack. Soluble CD39 is also useful for preventing
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC	restenosis of blood vessels or stroke.
XX	Sequence 473 AA;
XX	Sequence 473 AA;

	Query Match Similarity	78.1%	Score 75:	DB 21:	Length 473:
	Best Local Similarity	73.7%	Pred. No.	0.00012:	
	Matches 14:	Conservative	4:	Mismatches	1:
				Indels	0:
				Gaps	0:

QY	1 KSDTGETYGALDLCAGSTQ I9
	:::
Db	199 ETNNETFGALDLGCASTQ 217

	RESULT 12
AAY70900	ID
AAY70900	standard; Protein; 474 AA.
XX AC	
XX AC	AAY70900;
XX DT	17-AUG-2000 (first entry)
XX DE	
DE	Protein encoded by Trtm 3 construct.
XX XX	
KM	Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KM	unstable angina; myocardial infarction; stroke; coronary artery disease;
KM	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KM	platelet-associated ischemic disorder; lung ischaemia; thrombolytic;
KM	cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KM	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KM	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KM	PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KM	occlusion; reocclusion; stenosis; restenosis; antiangiogenic; cardiatic;
KM	cerebroprotective; antithrombotic; vasodilator; anticoagulant;
KM	coronary ischaemia; vascular occlusion; piliTrtm3 variant.
XX OS	Homo sapiens.
OS	Synthetic.
XX XX	
FH	Key
FT	Cleavage-site
FT FT	24..25
FT	Protein
XX XX	note= "Soluble portion of CD39"
PN	WO200023094-A2.
XX XX	
XX PD	27-APR-2000.
PD	
PF	13-OCT-1999; 99MO-US2364.1.
XX PR	16-OCT-1998; 98US-0104565.
PR	06-NOV-1998; 98US-0107466.
PR PR	13-AUG-1999; 99US-0149010.
XX XX	
PA	(IMMV) IMMUNEX CORP.
PA	(CORR) CORNELL RES FOUND INC.
PI PI	Maliszewski CR, Gayle RB, Marcus AJ;
XX DR	
DR	WPI; 2000-339518/29.
PT	Inhibiting platelet activation and recruitment, useful for treating a
PT	mammal suffering from unstable angina, myocardial infarction, stroke,
PT	coronary artery disease or injury, comprises administering soluble CD39
PM	polypeptides -
XX XX	
PS	Example 11: Page 113-114; 118pp; English.
XX XX	
CC	The present sequence is the protein encoded by Trtm3 construct, piliTrtm3
CC	variant was constructed by removing the human IL2 residues from solCD39
CC	fusion construct. Fusion of 12 amino acids from the N-terminus of mature
CC	human IL2 to the solCD39 coding region results in high levels of both
CC	expression and activity in the supernatants of transfected cells. SolCD39
CC	is used in the treatment of unstable angina, myocardial infarction,
CC	stroke, coronary artery disease or injury, atherosclerosis, peripheral
CC	vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
CC	disorder including lung ischaemia, coronary ischaemia and cerebral

The present sequence is the fusion protein construct, PIL2LTrim3. This

2A (IMMV) IMMUNEX CORP.
2A (CORR) CORNELL RES FOUND INC

XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI: 2000-339518/29.
 XX
 PT Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 PS
 PS Claim 6; Page 89-91; 118pp; English.
 XX
 XX The present sequence is a fusion construct of human soluble CD39 encoded
 CC by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the
 CC CD39 family. The fusion construct is used for the expression and activity
 CC of soluble CD39 in CHO (chinese hamster ovary) cells. Soluble CD39
 CC retains the capacity of wildtype CD39 to metabolise ATP and ADP at
 CC physiologically relevant concentrations as well as the ability to block
 CC and reverse ADP-induced platelet activation and recruitment including
 CC platelet aggregation. This is used in the treatment of unstable angina,
 CC myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.
 XX
 XX Sequence 476 AA;
 SQ
 Query Match 78.1%; Score 75; DB 21; Length 476;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KSDQETRYGALDLGASSTQ 19
 DB 202 ETNNQETFGALDLGASSTQ 220
 RESULT 15
 AAY70889
 ID AAY70889 standard: Protein: 476 AA.
 XX
 AC AAY70889;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by CD39-L4 construct.
 XX
 XX Soluble CD39: ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
 KW coronary ischaemia; cerebral ischaemia; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;
 KW thrombotic disorder; vascular occlusion.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT MISC-difference 39 /note= "Any amino acid preferably Cys or Ser"
 FT Cleavage-site 20..21
 FT Region 1..48
 FT /note= "Derived from CD39-L4"

FT Region 49..476
 FT /note= "Soluble portion of CD39"
 XX
 XX W0200023094-A2.
 XX
 PD 27-APR-2000.
 XX
 PF 13-OCT-1999; 99W0-US23641.
 XX
 PR 16-OCT-1998; 98US-0104595.
 PR 06-NOV-1998; 98US-0107466.
 PR 13-AUG-1999; 99US-0149010.
 XX
 PA (IMVU) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Maliszewski CR, Gayle RB, Marcus AJ;
 XX
 XX WPI: 2000-339518/29.
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 XX
 XX Claim 6; Page 91-93; 118pp; English.
 XX
 XX The present sequence is a fusion construct of human soluble CD39 encoded
 CC by CD39-L4-2 and CD39-L4-3 constructs. CD39-L4 is a secreted apyrase
 CC belonging to the CD39 family. The fusion construct is used for the
 CC expression and activity of soluble CD39 in CHO (chinese hamster ovary)
 CC cells. Soluble CD39 retains the capacity of wildtype CD39 to metabolise
 CC ATP and ADP at physiologically relevant concentrations as well as the
 CC ability to block and reverse ADP-induced platelet activation and
 CC recruitment including platelet aggregation. This is used in the treatment
 CC of unstable angina, myocardial infarction, stroke, coronary artery
 CC disease or injury, atherosclerosis, peripheral vascular occlusion,
 CC preclampsia, embolism, platelet-associated ischaemic disorder including
 CC lung ischaemia, coronary artery thrombosis, cerebral artery
 CC disorder including coronary artery thrombosis, peripheral artery
 CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
 CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
 CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
 CC useful for preventing thrombus formation or reformation, occlusion,
 CC reocclusion, stenosis or restenosis of blood vessels or stroke.
 XX
 XX Sequence 476 AA;
 SQ
 Query Match 78.1%; Score 75; DB 21; Length 476;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KSDQETRYGALDLGASSTQ 19
 DB 202 ETNNQETFGALDLGASSTQ 220

Search completed: February 11, 2003, 18:37:42
 Job time : 83 secs

100

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Scientific & Technical Informa

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech searcher* who conducted the search or contact:

Mary Hale, Supervisor, 301
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

1

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:36:22 ; Search time 30 Seconds
(without alignments)
18,635 Million cell updates/sec

Title: US-09-781-796B-7

Perfect score: 96
Sequence: 1 KSDQETGALDLCGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:*

- 1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCYTUS.COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	20	4 US-08-930-921-7	Sequence 7, Appl
2	82	85.4	16	4 US-08-930-921-8	Sequence 8, Appl
3	75	78.1	510	4 US-08-930-921-1	Sequence 1, Appl
4	64	66.7	405	4 US-09-608-285A-25	Sequence 25, Appl
5	64	66.7	405	4 US-09-370-265-25	Sequence 25, Appl
6	64	66.7	428	4 US-09-608-285A-3	Sequence 3, Appl
7	64	66.7	428	4 US-09-608-285A-5	Sequence 5, Appl
8	64	66.7	428	4 US-09-608-285A-7	Sequence 7, Appl
9	64	66.7	428	4 US-09-240-639-6	Sequence 6, Appl
10	64	66.7	428	4 US-09-240-639-9	Sequence 9, Appl
11	64	66.7	428	4 US-09-350-836B-3	Sequence 3, Appl
12	64	66.7	428	4 US-09-350-836B-5	Sequence 5, Appl
13	64	66.7	428	4 US-09-350-836B-7	Sequence 7, Appl
14	64	66.7	428	4 US-09-370-265-3	Sequence 3, Appl
15	64	66.7	428	4 US-09-370-265-5	Sequence 5, Appl
16	64	66.7	428	4 US-09-370-265-7	Sequence 7, Appl
17	64	66.7	428	4 US-09-240-639-8	Sequence 8, Appl
18	64	66.7	428	4 US-09-240-639-4	Sequence 4, Appl
19	62	50.0	428	4 US-09-129-112-2	Sequence 2, Appl
20	46	47.9	428	4 US-09-240-639-2	Sequence 2, Appl
21	46	47.9	428	4 US-09-608-285A-60	Sequence 60, Appl
22	46	47.9	428	4 US-09-608-285A-27	Sequence 27, Appl
23	46	47.9	428	4 US-09-370-265-27	Sequence 27, Appl
24	46	47.9	428	4 US-09-240-639-10	Sequence 10, Appl
25	43	44.8	428	4 US-09-129-112-15	Sequence 15, Appl
26	41	42.7	428	4 US-09-240-639-11	Sequence 11, Appl
27	40.5	42.2	428	4 US-09-129-112-9	Sequence 9, Appl

28	39	40.6	473	4 US-09-240-639-12	Sequence 12, Appl
29	38	39.6	31	4 US-08-905-223-410	Sequence 410, Appl
30	38	39.6	69	1 US-08-446-692-95	Sequence 95, Appl
31	38	39.6	69	2 US-08-446-692-95	Sequence 95, Appl
32	38	39.6	332	2 US-08-637-763B-6	Sequence 6, Appl
33	38	39.6	332	3 US-09-170-354-6	Sequence 6, Appl
34	38	39.6	386	1 US-08-319-621A-14	Sequence 14, Appl
35	38	39.6	649	4 US-09-066-047-5	Sequence 5, Appl
36	38	39.6	678	5 PCT-US93-03027-3	Sequence 3, Appl
37	37	38.5	346	4 US-09-343-011B-2	Sequence 2, Appl
38	37	38.5	361	4 US-09-655-270A-21	Sequence 21, Appl
39	37	38.5	366	4 US-09-651-941-25	Sequence 25, Appl
40	37	38.5	366	4 US-09-955-597-25	Sequence 25, Appl
41	37	38.5	425	4 US-08-134-001C-5619	Sequence 5619, Appl
42	37	38.5	467	4 US-09-129-112-19	Sequence 19, Appl
43	36.5	38.0	1548	4 US-09-376-330-15	Sequence 15, Appl
44	36	37.5	40	3 US-08-926-842B-51	Sequence 51, Appl
45	36	37.5	123	2 US-08-665-202-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-08-930-921-7
: Sequence 7, Application US/08930921B
: Patent No. 6287837
: GENERAL INFORMATION:
: APPLICANT: BEAUDOIN, Adrien R.
: APPLICANT: SEVIGNY, Jean
: TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
: TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
: FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
: CURRENT APPLICATION NUMBER: US/08/930,921B
: EARLIER FILING DATE: 1998-01-02
: EARLIER FILING DATE: 1996-04-10
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: unknown
: US-08-930-921-7

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Best local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDQETGALDLCGASTQ 19
Db 1 KSDQETGALDLCGASTQ 19

RESULT 2
US-08-930-921-8
: Sequence 8, Application US/08930921B
: Patent No. 6287837
: GENERAL INFORMATION:
: APPLICANT: BEAUDOIN, Adrien R.
: APPLICANT: SEVIGNY, Jean
: TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
: TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
: FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
: CURRENT APPLICATION NUMBER: US/08/930,921B
: EARLIER FILING DATE: 1998-01-02
: EARLIER FILING DATE: 1996-04-10
: NUMBER OF SEQ ID NOS: 8

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* SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-8

Query Match
Best Local Similarity 85.4%; Score 82; DB 4; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGGA 16
DB 1 KSDTQETYGALDLGGA 16

RESULT 3
US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1998-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1

Query Match
Best Local Similarity 78.1%; Score 75; DB 4; Length 510;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGASTQ 19
DB 202 ETNQTETGALDLGASTQ 220

RESULT 4
US-09-608-285A-25
; Sequence 25, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Teung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
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; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-25

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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

RESULT 5
US-09-370-265-25
; Sequence 25, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-25

Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 405;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

RESULT 6
US-09-608-285A-3
; Sequence 3, Application US/09608285A
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Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDYGASTQ 19
DB 192 QETVGTLDYGASTQ 206

RESULT 7
US-09-608-285A-5
Sequence 5, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDYGASTQ 19
DB 192 QETVGTLDYGASTQ 206

PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-5

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDYGASTQ 19
DB 192 QETVGTLDYGASTQ 206

RESULT 8
US-09-608-285A-7
Sequence 7, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDYGASTQ 19
DB 192 QETVGTLDYGASTQ 206

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RESULT 9
US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-6

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 QETYGALDLCGASTQ 19
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Db 192 QETVGTLDLCGASTQ 206

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RESULT 10
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-9

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 QETYGALDLCGASTQ 19
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Db 192 QETVGTLDLCGASTQ 206

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RESULT 11
US-09-350-836B-3
; Sequence 3, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19

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; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-3

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 QETYGALDLCGASTQ 19
||| | |||||
Db 192 QETVGTLDLCGASTQ 206

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RESULT 12
US-09-350-836B-5
; Sequence 5, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-5

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 QETYGALDLCGASTQ 19
||| | |||||
Db 192 QETVGTLDLCGASTQ 206

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RESULT 13
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447

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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
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; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 7
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; ORGANISM: Homo sapiens
US-09-350-836b-7
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Query Match 66.7%: Score 64; DB 4; Length 428;
Best Local Similarity 86.7%: Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206
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RESULT 14
US-09-370-265-3
; Sequence 3, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
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; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-3
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Query Match 66.7%: Score 64; DB 4; Length 428;
Best Local Similarity 86.7%: Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206
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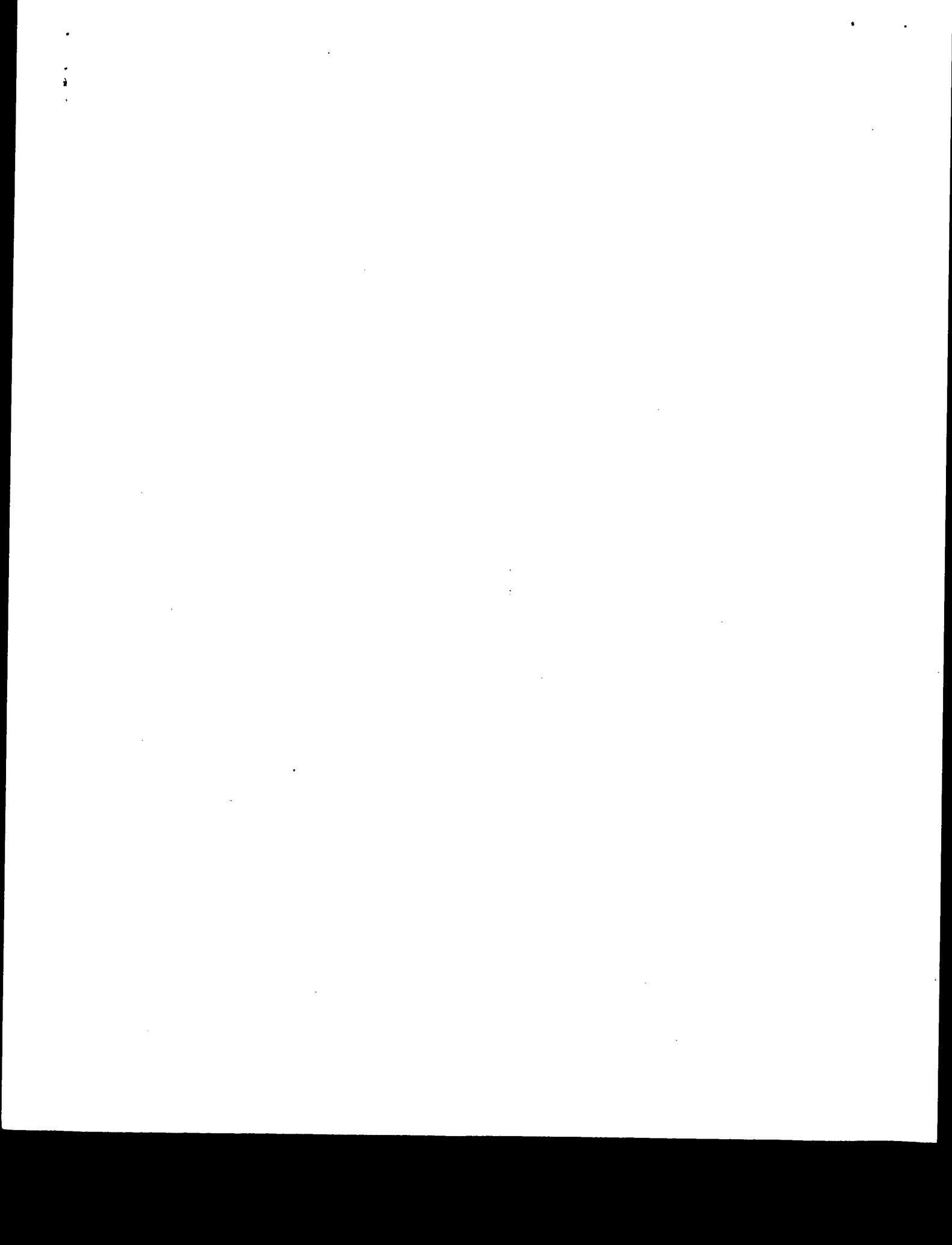
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US-09-370-265-5
; Sequence 5, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
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; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-5
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Query Match 66.7%: Score 64; DB 4; Length 428;
Best Local Similarity 86.7%: Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206
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Job time : 32 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 18:39:47 ; Search time 12 Seconds
(without alignments)
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Title: US-09-781-796b-7
Perfect score: 96
Sequence: 1 KSDTQETGALDGGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 140259 seqs, 2554876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	78.1	439	10	US-09-374-586-2
2	75	78.1	454	10	US-09-835-147-6
3	75	78.1	463	10	US-09-835-147-30
4	75	78.1	464	10	US-09-835-147-27
5	75	78.1	473	10	US-09-835-147-29
6	75	78.1	474	10	US-09-835-147-28
7	75	78.1	476	10	US-09-835-147-3
8	75	78.1	476	10	US-09-835-147-4
9	75	78.1	478	10	US-09-835-147-8
10	75	78.1	487	10	US-09-835-147-26
11	75	78.1	502	9	US-10-092-063-38
12	75	78.1	510	10	US-09-835-147-2
13	75	78.1	510	10	US-09-374-586-1
14	75	78.1	505	10	US-10-092-063-25
15	64	66.7	405	9	US-10-092-063-3
16	64	66.7	428	9	US-10-092-063-5
17	64	66.7	428	9	US-10-092-063-7
18	64	66.7	428	12	US-10-091-085-3
19	64	66.7	428	12	US-10-091-085-5

20	64	66.7	428	12	US-10-091-085-7	Sequence 7, Appl1
21	64	66.7	465	9	US-10-092-063-39	Sequence 39, Appl1
22	62	64.6	529	10	US-09-823-304-4	Sequence 4, Appl1
23	60	62.5	330	10	US-09-823-299-876	Sequence 876, App
24	52	54.2	458	9	US-10-174-590-436	Sequence 496, App
25	52	54.2	458	9	US-10-176-758-496	Sequence 496, App
26	52	54.2	458	9	US-10-175-737-496	Sequence 496, App
27	52	54.2	458	9	US-10-173-706-496	Sequence 496, App
28	52	54.2	458	9	US-10-175-738-496	Sequence 496, App
29	52	54.2	458	9	US-10-175-732-496	Sequence 496, App
30	52	54.2	458	9	US-10-176-482-496	Sequence 496, App
31	52	54.2	458	9	US-10-176-757-496	Sequence 496, App
32	52	54.2	458	9	US-10-176-913-496	Sequence 496, App
33	52	54.2	458	9	US-10-180-552-496	Sequence 496, App
34	52	54.2	458	9	US-10-180-557-496	Sequence 496, App
35	52	54.2	458	9	US-10-173-700-496	Sequence 496, App
36	52	54.2	458	9	US-10-174-572-496	Sequence 496, App
37	52	54.2	458	9	US-10-174-579-496	Sequence 496, App
38	52	54.2	458	9	US-10-174-582-496	Sequence 496, App
39	52	54.2	458	9	US-10-175-588-496	Sequence 496, App
40	52	54.2	458	9	US-10-175-739-496	Sequence 496, App
41	52	54.2	458	9	US-10-175-740-496	Sequence 496, App
42	52	54.2	458	9	US-10-175-743-496	Sequence 496, App
43	52	54.2	458	9	US-10-176-488-496	Sequence 496, App
44	52	54.2	458	9	US-10-176-492-496	Sequence 496, App
45	52	54.2	458	9	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-09-374-586-2
Sequence 2, Application US/09374586
Patient No. US20020138858A1
GENERAL INFORMATION:
APPLICANT: Phisiky, David J.
TITLE OF INVENTION: CD39/EC70-ADPASE AS A TREATMENT FOR THROMBOTIC AND
FILE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374, 586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 78.1%; Score 75; DB 10; Length 439;
Best Local Similarity 73.7%; Pred. 4.2e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDGGASTQ 19
Db 165 ETNNGETGALDGGASTQ 183
RESULT 2
US-09-835-147-6
Sequence 6, Application US/09835147
Patient No. US20020002277A1
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835, 147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104, 585

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; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

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Query Match      78.1%; Score 75; DB 10; Length 454;
Best Local Similarity 73.7%; Pred. No. 4.4e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 1 KSDTQETYGALDGGASTQ 19
Db 180 ETNNOETFGALDGGASTQ 198

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RESULT 3
US-09-835-147-30
; Sequence 30; Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

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Query Match      78.1%; Score 75; DB 10; Length 463;
Best Local Similarity 73.7%; Pred. No. 4.5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDTQETYGALDGGASTQ 19
Db 189 ETNNOETFGALDGGASTQ 207

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RESULT 4
US-09-835-147-27
; Sequence 27; Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:

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; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

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Query Match      78.1%; Score 75; DB 10; Length 464;
Best Local Similarity 73.7%; Pred. No. 4.5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db 190 ETNNOETFGALDGGASTQ 208

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RESULT 5
US-09-835-147-29
; Sequence 29; Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

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Query Match      78.1%; Score 75; DB 10; Length 473;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDTQETYGALDGGASTQ 19

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Db 199 ETNNQETFGALDLGASTQ 217

RESULT 6
US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 78.1%; Score 75; DB 10; Length 474;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETFGALDLGASTQ 19
Db 200 ETNNQETFGALDLGASTQ 218

RESULT 7
US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-3

Query Match 78.1%; Score 75; DB 10; Length 476;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETFGALDLGASTQ 19
Db 202 ETNNQETFGALDLGASTQ 220

RESULT 8
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 78.1%; Score 75; DB 10; Length 476;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETFGALDLGASTQ 19
Db 202 ETNNQETFGALDLGASTQ 220

RESULT 9
US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466

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Db      202 ETNNQETFGALDLGASTQ 220
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RESULT 13
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Plinsky, David J.
; TITLE OF INVENTION: CD39/ECMO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match          78.1%; Score 75; DB 10; Length 510;
Best Local Similarity 73.7%; Pred. No. 5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSDQETGYALDGGASTQ 19
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Db      202 ETNNGETFGALDGGASTQ 220

RESULT 14
US-10-092-063-25
; Sequence 25, Application US/10092063
; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-25

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Best Local Similarity 86.7%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 QETGYALDGGASTQ 19
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Db      192 QETVGTLDGGASTQ 206

RESULT 15
US-10-092-063-3
; Sequence 3, Application US/10092063

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; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-3

Query Match          66.7%; Score 64; DB 9; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 QETGYALDGGASTQ 19
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Db      192 QETVGTLDGGASTQ 206

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Job time : 13 secs

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:37:47 ; Search time 354 Seconds
(without alignments)
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Title: US-09-781-796b-7

Sequence: 1 KSDPTERYGALDLCGASTQ 19

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Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	82	85.4	16	21	US-09-781-796b-8
3	75	78.1	276	19	US-09-538-630A-30
4	75	78.1	439	1	PCT-US00-22060-2
5	75	78.1	439	17	US-09-374-586-2
6	75	78.1	454	1	PCT-US99-22955-6

7	75	78.1	454	22	US-09-807-660A-6	Sequence 6, Appl1
8	75	78.1	454	22	US-09-835-147-6	Sequence 6, Appl1
9	75	78.1	463	1	PCT-US99-22955-30	Sequence 30, Appl1
10	75	78.1	463	22	US-09-807-660A-30	Sequence 30, Appl1
11	75	78.1	463	22	US-09-835-147-30	Sequence 27, Appl1
12	75	78.1	464	1	PCT-US99-22955-27	Sequence 27, Appl1
13	75	78.1	464	22	US-09-807-660A-27	Sequence 27, Appl1
14	75	78.1	464	22	US-09-835-147-27	Sequence 29, Appl1
15	75	78.1	473	1	PCT-US99-22955-29	Sequence 29, Appl1
16	75	78.1	473	22	US-09-807-660A-29	Sequence 29, Appl1
17	75	78.1	473	22	US-09-835-147-29	Sequence 28, Appl1
18	75	78.1	474	1	PCT-US99-22955-28	Sequence 28, Appl1
19	75	78.1	474	22	US-09-835-147-28	Sequence 28, Appl1
20	75	78.1	474	22	US-09-835-147-28	Sequence 28, Appl1
21	75	78.1	476	1	PCT-US99-22955-3	Sequence 3, Appl1
22	75	78.1	476	22	US-09-807-660A-3	Sequence 3, Appl1
23	75	78.1	476	22	US-09-807-660A-4	Sequence 3, Appl1
24	75	78.1	476	22	US-09-835-147-3	Sequence 3, Appl1
25	75	78.1	476	22	US-09-835-147-3	Sequence 4, Appl1
26	75	78.1	478	1	PCT-US99-22955-8	Sequence 8, Appl1
27	75	78.1	478	22	US-09-807-660A-8	Sequence 8, Appl1
28	75	78.1	478	22	US-09-835-147-8	Sequence 26, Appl1
29	75	78.1	487	1	PCT-US99-22955-26	Sequence 26, Appl1
30	75	78.1	487	22	US-09-807-660A-26	Sequence 26, Appl1
31	75	78.1	487	22	US-09-835-147-26	Sequence 38, Appl1
32	75	78.1	502	17	US-09-370-625A-38	Sequence 38, Appl1
33	75	78.1	502	19	US-09-557-800C-55	Sequence 38, Appl1
34	75	78.1	502	24	US-10-092-063-38	Sequence 1, Appl1
35	75	78.1	510	1	PCT-US00-22060-1	Sequence 2, Appl1
36	75	78.1	510	1	PCT-US99-22955-2	Sequence 2, Appl1
37	75	78.1	510	11	US-08-701-460-2	Sequence 2, Appl1
38	75	78.1	510	11	US-08-701-460-4	Sequence 1, Appl1
39	75	78.1	510	11	US-09-374-586-1	Sequence 1, Appl1
40	75	78.1	510	21	US-09-781-796b-1	Sequence 2, Appl1
41	75	78.1	510	22	US-09-807-660A-2	Sequence 2, Appl1
42	75	78.1	510	22	US-09-835-147-2	Sequence 2, Appl1
43	75	78.1	510	22	US-09-834-366-17025	Sequence 17025, A
44	69	71.9	120	22	US-09-834-366-17027	Sequence 17027, A
45	69	71.9	120	22	US-09-834-366-17027	Sequence 17027, A

ALIGNMENTS

RESULT 1
US-09-781-796b-7
US-09-781-796b-7 Application US/09781796B
GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SVIGNY, Jean
APPLICANT: BACH, Fritz H.
APPLICANT: ROBSON, Simon
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TECHNOLOGY
FILE REFERENCE: 920333.90019
CURRENT APPLICATION NUMBER: US/09/781,796B
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR APPLICATION NUMBER: CA96/00223
PRIOR FILING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: 08/930,921
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 19
TYPE: PRT
ORGANISM: Porcine
US-09-781-796b-7
Query Match 100.0%; Score 96; DB 21; Length 19;

Best Local Similarity 100.0%; Pred. No. 3 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDTOETFGALDLAGASTQ 19
Db 1 KSDTOETFGALDLAGASTQ 19

RESULT 2

US-09-781-796b-8
Sequence 8, Application US/09781796B
GENERAL INFORMATION:

APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SVIGNY, Jean
APPLICANT: BACH, Fritz H.
APPLICANT: ROBSON, Simon
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
FILE REFERENCE: 920333.90019
CURRENT APPLICATION NUMBER: US/09/781,796B
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR APPLICATION NUMBER: CA96/00223
PRIOR FILING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: 08/930,921
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 16
TYPE: PRT
ORGANISM: Human and bovine
US-09-781-796b-8

Query Match

Best Local Similarity 85.4%; Score 82; DB 21; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDTOETFGALDLAGA 16
Db 1 KSDTOETFGALDLAGA 16

RESULT 3

US-09-558-630A-30
Sequence 30, Application US/09558630A
GENERAL INFORMATION:

APPLICANT: MINTZ, Liat et al.
TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0150P
CURRENT APPLICATION NUMBER: US/09/558,630A
CURRENT FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-558-630A-30

Query Match

Best Local Similarity 78.1%; Score 75; DB 19; Length 276;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTOETFGALDLAGASTQ 19
Db 202 ETNNOETFGALDLAGASTQ 220

RESULT 4
PCT-US00-22060-2

Sequence 2, Application PC/TUS0022060
GENERAL INFORMATION:

APPLICANT: Pinsky, David J.
TITLE OF INVENTION: CD39/ECCTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
TITLE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: PCT/US00/22060
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-22060-2

Query Match

Best Local Similarity 78.1%; Score 75; DB 1; Length 439;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTOETFGALDLAGASTQ 19
Db 165 ETNNOETFGALDLAGASTQ 183

RESULT 5

US-09-374-586-2
Sequence 2, Application US/09374586
GENERAL INFORMATION:

APPLICANT: Pinsky, David J.
TITLE OF INVENTION: CD39/ECCTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
TITLE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
US-09-374-586-2

Query Match

Best Local Similarity 78.1%; Score 75; DB 17; Length 439;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTOETFGALDLAGASTQ 19
Db 165 ETNNOETFGALDLAGASTQ 183

RESULT 6

PCT-US99-22955-6
Sequence 6, Application PC/TUS9922955
GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
PCT-US99-22955-6

Query Match 78.1%; Score 75; DB 1; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 7
US-09-807-660A-6
Sequence 6, Application US/09807660A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Marcus, Aaron J.
APPLICANT: ImmuneX Corporation
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
FILE REFERENCE: 23,495 PCT
CURRENT APPLICATION NUMBER: US/09/807,660A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
US-09-807-660A-6

Query Match 78.1%; Score 75; DB 22; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 8
US-09-835-147-6
Sequence 6, Application US/09835147
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 78.1%; Score 75; DB 22; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 9
PCT-US99-22955-30
Sequence 30, Application PC/TUS9922955
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: ImmuneX Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 463
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
PCT-US99-22955-30

Query Match 78.1%; Score 75; DB 1; Length 463;
Best Local Similarity 73.7%; Pred. No. 0.00081;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 189 ETNNQETFGALDLCGASTQ 207

RESULT 10
US-09-807-660A-30
Sequence 30, Application US/09807660A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Marcus, Aaron J.
APPLICANT: ImmuneX Corporation
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
FILE REFERENCE: 23,495 PCT

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; CURRENT APPLICATION NUMBER: US/09/807,660A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-807-660A-30
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Query Match
Best Local Similarity 78.1%; Score 75; DB 22; Length 463;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KSDQETFGALDGLGASTQ 19
DB 189 ETNNOETFGALDGLGASTQ 207
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RESULT 11

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US-09-835-147-30
; Sequence 30, Application US/09835147
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Steven D.
; APPLICANT: Gimpel, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30
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Query Match
Best Local Similarity 78.1%; Score 75; DB 22; Length 463;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSDQETFGALDGLGASTQ 19
DB 189 ETNNOETFGALDGLGASTQ 207
```

```
RESULT 12
PCT-US99-22955-27
; Sequence 27, Application PC/TUS9922955
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
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; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; APPLICANT: Immune Corporation
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-WO
; CURRENT APPLICATION NUMBER: PCT/US99/22955
; CURRENT FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 60/104,585
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: US 60/107,466
; EARLIER FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/149,010
; EARLIER FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
PCT-US99-22955-27
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Query Match
Best Local Similarity 78.1%; Score 75; DB 1; Length 464;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
OY 1 KSDQETFGALDGLGASTQ 19
DB 190 ETNNOETFGALDGLGASTQ 208
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RESULT 13

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US-09-807-660A-27
; Sequence 27, Application US/09807660A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Marcus, Aaron J.
; APPLICANT: Immune Corporation
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
; FILE REFERENCE: 23,495 PCT
; CURRENT APPLICATION NUMBER: US/09/807,660A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-807-660A-27
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Query Match
Best Local Similarity 78.1%; Score 75; DB 22; Length 464;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
OY 1 KSDQETFGALDGLGASTQ 19
DB 190 ETNNOETFGALDGLGASTQ 208
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RESULT 14
US-09-835-147-27
Sequence 27, Application US/09835147

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

PRIOR FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-10-16

PRIOR APPLICATION NUMBER: US 60/107,466

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: US 60/149,010

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 27

LENGTH: 464

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion

OTHER INFORMATION: construct of human CD39

US-09-835-147-27

Query Match

Best Local Similarity 78.1%; Score 75; DB 22; Length 464;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLDGASTQ 19

DB 190 ETNNOETFGALDLDGASTQ 208

RESULT 15

PCT-US99-22955-29

Sequence 29, Application PC/TUS9922955

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-10-16

PRIOR APPLICATION NUMBER: US 60/107,466

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: US 60/149,010

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 473

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion

OTHER INFORMATION: construct of human CD39

PCT-US99-22955-29

Query Match

Best Local Similarity 78.1%; Score 75; DB 1; Length 473;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLDGASTQ 19

DB 199 ETNNOETFGALDLDGASTQ 217

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLDGASTQ 19

DB 199 ETNNOETFGALDLDGASTQ 217

Search completed: February 11, 2003, 18:46:40
Job time : 355 secs

11

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:38:07 : Search time 19 Seconds
(without alignments)
83.231 Million cell updates/sec

Title: US-09-781-796b-7
Perfect score: 96
Sequence: 1 KSDQETFGALDGGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 420401 seqs, 83231269 residues

Total number of hits satisfying chosen parameters: 420401

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/us06_NEW.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	78.1	276	5 US-09-724-676-59001	Sequence 59001, A
2	75	78.1	276	5 US-09-724-676-59001	Sequence 59001, A
3	75	78.1	283	5 US-09-724-676-59000	Sequence 59000, A
4	75	78.1	283	5 US-09-724-676-59000	Sequence 59000, A
5	75	78.1	439	6 US-10-049-420-2	Sequence 2, App1
6	75	78.1	454	5 US-09-835-147A-6	Sequence 6, App1
7	75	78.1	464	5 US-09-835-147A-30	Sequence 3, App1
8	75	78.1	464	5 US-09-835-147A-27	Sequence 27, App1
9	75	78.1	473	5 US-09-835-147A-29	Sequence 29, App1
10	75	78.1	474	5 US-09-835-147A-28	Sequence 28, App1
11	75	78.1	476	5 US-09-835-147A-3	Sequence 3, App1
12	75	78.1	476	5 US-09-835-147A-4	Sequence 4, App1
13	75	78.1	478	5 US-09-835-147A-8	Sequence 8, App1
14	75	78.1	487	5 US-09-835-147A-26	Sequence 26, App1
15	75	78.1	510	5 US-09-835-147A-2	Sequence 2, App1
16	75	78.1	510	6 US-10-049-420-1	Sequence 1, App1
17	75	78.1	517	5 US-09-724-676-58998	Sequence 58998, A
18	75	78.1	517	5 US-09-724-676-58999	Sequence 58999, A
19	75	78.1	517	5 US-09-724-676-58998	Sequence 58998, A
20	75	78.1	517	5 US-09-724-676-58999	Sequence 58999, A
21	58	60.4	701	6 US-10-310-154-534	Sequence 534, App
22	52	54.2	458	1 PCT-US02-40161-16	Sequence 16, App
23	52	54.2	458	1 PCT-US02-40161-30	Sequence 30, App
24	52	54.2	458	6 US-10-125-923A-496	Sequence 496, App
25	52	54.2	458	6 US-10-205-892-496	Sequence 496, App
26	52	54.2	458	6 US-10-174-575-496	Sequence 496, App

27	52	54.2	458	6 US-10-174-575A-496	Sequence 496, App
28	52	54.2	458	6 US-10-187-755-496	Sequence 496, App
29	52	54.2	458	6 US-10-187-749-496	Sequence 496, App
30	52	54.2	458	6 US-10-199-672-496	Sequence 496, App
31	47	49.0	435	5 US-09-724-676-76017	Sequence 76017, A
32	47	49.0	435	5 US-09-724-676-76017	Sequence 76017, A
33	47	49.0	451	5 US-09-724-676-76019	Sequence 76019, A
34	47	49.0	451	5 US-09-724-676-76019	Sequence 76019, A
35	47	49.0	594	5 US-09-724-676-76016	Sequence 76016, A
36	47	49.0	594	5 US-09-724-676-76016	Sequence 76016, A
37	47	49.0	602	5 US-09-724-676-76018	Sequence 76018, A
38	47	49.0	602	5 US-09-724-676-76018	Sequence 76018, A
39	46	47.9	282	5 US-09-724-676-59094	Sequence 59094, A
40	46	47.9	282	5 US-09-724-676-59094	Sequence 59094, A
41	46	47.9	402	5 US-09-724-676-59085	Sequence 59085, A
42	46	47.9	402	5 US-09-724-676-59085	Sequence 59085, A
43	46	47.9	402	5 US-09-724-676-59088	Sequence 59088, A
44	46	47.9	402	5 US-09-724-676-59088	Sequence 59088, A
45	46	47.9	402	5 US-09-724-676A-59085	Sequence 59085, A

ALIGNMENTS

RESULT 1
US-09-724-676-59001
Sequence 59001, Application US/09724676
GENERAL INFORMATION: LTD
APPLICANT: CompuGen
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 CompuGen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 59001
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-59001

Query Match 78.1%; Score 75; DB 5; Length 276;
Best Local Similarity 73.7%; Pred. No. 0.00013;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDGGASTQ 19
DB 202 ETNQETFGALDGGASTQ 220

RESULT 2
US-09-724-676A-59001
Sequence 59001, Application US/09724676A
GENERAL INFORMATION: LTD
APPLICANT: CompuGen
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 CompuGen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 59001
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-59001

Query Match 78.1%; Score 75; DB 5; Length 276;
Best Local Similarity 73.7%; Pred. No. 0.00013;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDQETFGALDGGASTQ 19
::: |||:|||||||

Db 202 ETNNQETFGALDGGASTQ 220

RESULT 3

US-09-724-676-59000
; Sequence 59000, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59000
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-59000

Query Match

Best Local Similarity 78.1%; Score 75; DB 5; Length 283;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 209 ETNNQETFGALDGGASTQ 227

RESULT 4

US-09-724-676A-59000
; Sequence 59000, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59000
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-59000

Query Match

Best Local Similarity 78.1%; Score 75; DB 5; Length 283;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 209 ETNNQETFGALDGGASTQ 227

RESULT 5

US-10-049-420-2
; Sequence 2, Application US/10049420
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECDO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/10/049,420
; CURRENT FILING DATE: 2002-02-06
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-049-420-2

Query Match
Best Local Similarity 78.1%; Score 75; DB 6; Length 439;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 165 ETNNQETFGALDGGASTQ 183

RESULT 6

US-09-835-147A-6
; Sequence 6, Application US/09835147A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-6

Query Match
Best Local Similarity 78.1%; Score 75; DB 5; Length 454;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 180 ETNNQETFGALDGGASTQ 198

RESULT 7

US-09-835-147A-30
; Sequence 30, Application US/09835147A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30

LENGTH: 463
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-30

Query Match 78.1%; Score 75; DB 5; Length 463;
Best Local Similarity 73.7%; Pred. No. 0.00022;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTOETYGALDYGASTQ 19
DB 189 ETNNOETFGALDYGASTQ 207

RESULT 8
US-09-835-147A-27
Sequence 27, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-27

Query Match 78.1%; Score 75; DB 5; Length 464;
Best Local Similarity 73.7%; Pred. No. 0.00022;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTOETYGALDYGASTQ 19
DB 190 ETNNOETFGALDYGASTQ 208

RESULT 9
US-09-835-147A-29
Sequence 29, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-29

Query Match 78.1%; Score 75; DB 5; Length 473;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTOETYGALDYGASTQ 19
DB 199 ETNNOETFGALDYGASTQ 217

RESULT 10
US-09-835-147A-28
Sequence 28, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 474
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-28

Query Match 78.1%; Score 75; DB 5; Length 474;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTOETYGALDYGASTQ 19
DB 200 ETNNOETFGALDYGASTQ 218

RESULT 11
US-09-835-147A-3
Sequence 3, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585

;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1998-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-3

Query Match 78.1%; Score 75; DB 5; Length 476;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDUGASTQ 19
Db 202 ETNNQETFGALDUGASTQ 220

RESULT 12
US-09-835-147A-4
;; Sequence 4, Application US/09835147A
;; GENERAL INFORMATION:
;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.
;; APPLICANT: Price, Virginia L.
;; APPLICANT: Gimpel, Steven D.
;; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
;; FILE REFERENCE: 2879-US
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: US 60/104,585
;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1998-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion construct of human CD39
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (39)..(39)
;; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147A-4

Query Match 78.1%; Score 75; DB 5; Length 476;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDUGASTQ 19
Db 202 ETNNQETFGALDUGASTQ 220

RESULT 13
US-09-835-147A-8
;; Sequence 8, Application US/09835147A
;; GENERAL INFORMATION:

;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.
;; APPLICANT: Price, Virginia L.
;; APPLICANT: Gimpel, Steven D.
;; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
;; FILE REFERENCE: 2879-US
;; CURRENT APPLICATION NUMBER: US/09/835,147A
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: US 60/104,585
;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1998-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 478
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-8

Query Match 78.1%; Score 75; DB 5; Length 478;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDUGASTQ 19
Db 204 ETNNQETFGALDUGASTQ 222

RESULT 14
US-09-835-147A-26
;; Sequence 26, Application US/09835147A
;; GENERAL INFORMATION:
;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.
;; APPLICANT: Price, Virginia L.
;; APPLICANT: Gimpel, Steven D.
;; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
;; FILE REFERENCE: 2879-US
;; CURRENT APPLICATION NUMBER: US/09/835,147A
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: US 60/104,585
;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1998-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 26
;; LENGTH: 487
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-26

Query Match 78.1%; Score 75; DB 5; Length 487;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDUGASTQ 19
Db 213 ETNNQETFGALDUGASTQ 231

RESULT 15
US-09-835

US-09-835-147A-2

US 05 055 147A 2
; Sequence 2, Application US/09835147A

; sequence 2, applicat
; GENERAL INFORMATION:

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; GENERAL INFORMATION:
;
; APPLICANT: Maliszewski, Charles R.

```

;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.

APPLICANT: Gayle III, Richard
APPLICANT: Price, Virginia L.

APPLICANT: Price, Virginia L.
APPLICANT: Gimbel, Steven D.

APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT

FILE REFERENCE. 2879-IIS

FILE REFERENCE: 2879-US
CURRENT ABJICATION NUMBER: US/09/A35 147A

CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2001-04-12

CURRENT FILING DATE: 2001-04-13

CONSENT FILING DATE: 2001 01 15
PRIOR APPLICATION NUMBER: US 61
; 1000 10 15

PRIOR FILING DATE: 1998-10-16

PRIOR FILING DATE: 1958 10 10
PRIOR APPLICATION NUMBER: US 6

;; PRIOR APPLICATION NUMBER: 05 80/101,400
;; PRIOR FILING DATE: 1998-11-06

;; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 6

;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/

PRIOR APPLICATION NUMBER: ;
PRIOR FILING DATE: 1999-11-11

PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS. 37

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

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; SEQ ID NO 2
;
; LENGTH: 510

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; LENGTH: 210
; TYPE: PRT
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US-09-835-147A-2
; ORGANISM: Homo sapiens

Query Match 78.1% Score 75 DB 5 Length 510

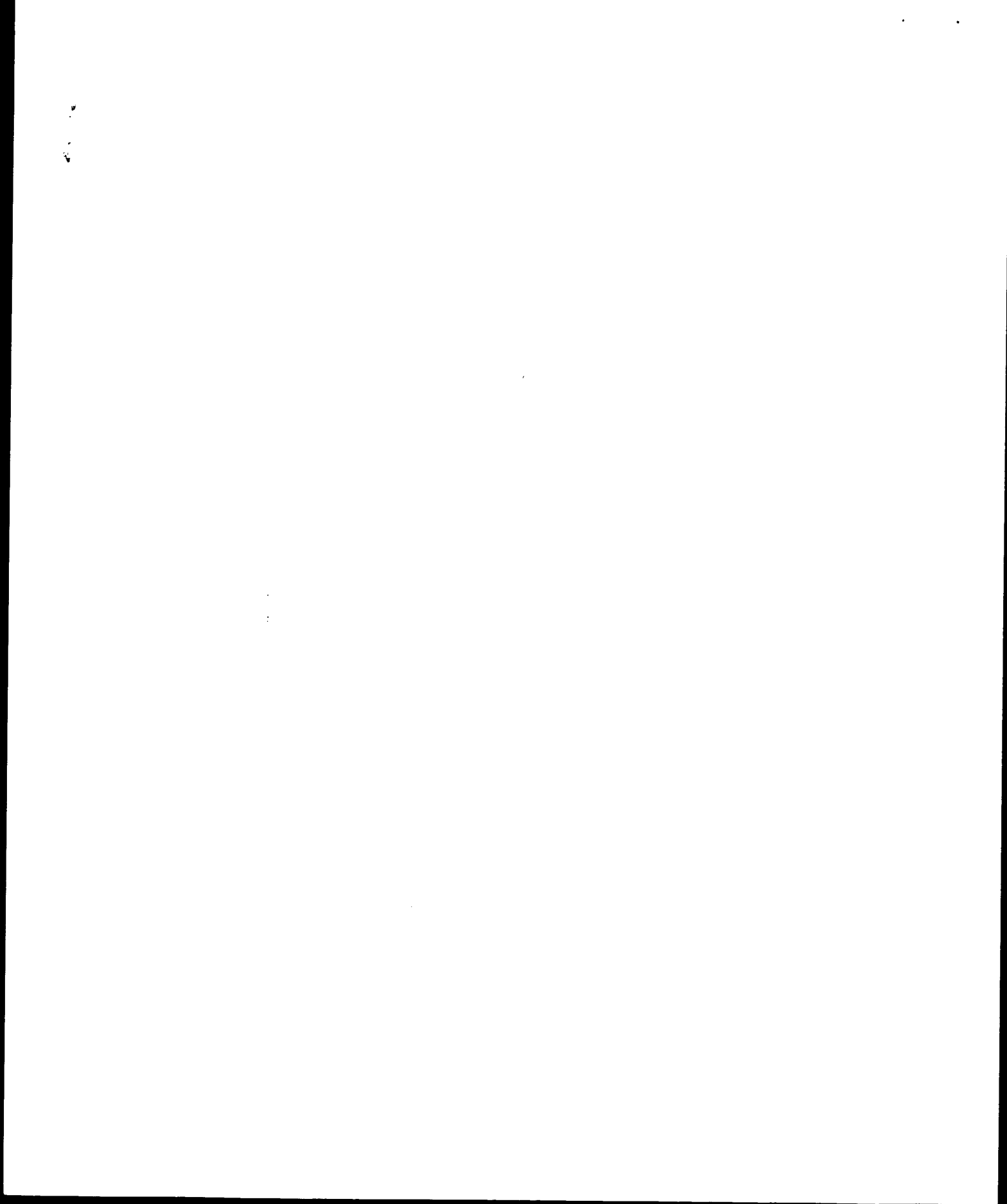
Query Match	78.18;	Score 75;	DB 5;
Best local similarity	73.78;	Pred. No.	0.00024;

Best Local Similarity 73.7%; Pred. No. 0.00024;
Matches 14: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

Matches 14; Conservative

Search completed: February 11, 2003, 18:47:06
Job time : 20 secs

Job time : 20 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:35:31 ; Search time 16 Seconds
(without alignments)
114.160 Million cell updates/sec

Title: US-09-781-796b-7

Sequence: 1 KSDPTQETFGALDLGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	78.1	510	2 156242	lymphoid cell acti
2	62	64.6	44	2 S63501	aprase (EC 3.6.1.
3	53	55.2	1052	2 T04439	hypothetical prote
4	52	54.2	630	2 S50463	hypothetical prote
5	51	53.1	556	2 T39109	probable guanosine
6	50	52.1	557	2 T16596	hypothetical prote
7	49	51.0	483	2 D86276	hypothetical prote
8	47	49.0	124	1 FAD02	profilin II - slim
9	46.5	48.4	572	2 T40856	probable nucleotid
10	44	45.8	263	2 C70741	hypothetical prote
11	44	45.8	377	2 S56505	hypothetical 41.9K
12	44	45.8	405	2 E86276	hypothetical prote
13	44	45.8	455	2 S48859	nucleoside triphos
14	44	45.8	516	2 G84442	probable nucleosid
15	44	45.8	925	2 S27920	nuclear antigen EB
16	43	44.8	494	2 D86493	polymorphic outer
17	43	44.8	534	2 JC5096	transposase - fung
18	42	43.8	421	2 T04798	hypothetical prote
19	42	43.8	479	2 T23508	hypothetical prote
20	41.5	43.2	293	2 H44644	botulinum neurotox
21	41	42.7	262	1 D69547	iron-sulfur cluste
22	41	42.7	416	2 A88109	protein C46E10.9 l
23	41	42.7	454	2 JCA616	aprase (EC 3.6.1.
24	41	42.7	470	2 A96286	propionyl coenzyme
25	41	42.7	510	2 AH2997	propionyl-coa carb
26	41	42.7	510	2 AC3352	transcription acti
27	41	42.7	519	2 A38073	probable mitogen a
28	41	42.7	677	2 T02951	conserved hypothet
29	40.5	42.2	809	2 F87458	

30	40	41.7	425	2 H70456	modulation competi
31	40	41.7	485	2 T34147	hypothetical prote
32	40	41.7	522	2 B71978	hypothetical prote
33	40	41.7	590	2 A40437	glutamic acid-rich
34	40	41.7	808	2 E64914	dimethylsulfoxide
35	40	41.7	828	2 F96535	hypothetical prote
36	40	41.7	884	2 A31928	glucose transport
37	39.5	41.1	463	1 T40661	mult protein C10
38	39	40.6	227	2 S77870	dnak-type molecula
39	39	40.6	294	2 B86703	tRNA isopentenyltr
40	39	40.6	294	2 G95077	tRNA isopentenyltr
41	39	40.6	311	2 D97945	tRNA isopentenyltr
42	39	40.6	315	2 F70203	xylose operon regu
43	39	40.6	505	1 S77034	protein kinase pkn
44	39	40.6	518	2 A40732	guanosine-diphosph
45	39	40.6	530	2 A87518	hypothetical prote

ALIGNMENTS

RESULT 1
156242
lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 156242
R:Maliszewski, C. R.; Delapessesse, G. J.; Schoenborn, M. A.; Arnltage, R. J.; Fanslow, W. C.
J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen, Molecular cloning and structural
A:Reference number: 156242; MUID:95015846; PMID:7930580
A:Accession: 156242
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: GB:S73813; NID:g765255; PIDN:AB32152.1; PID:g765256

Query Match 78.1% Score 75: DB 2: Length 510:
Best Local Similarity 73.7% Pred. No. 9e-05:
Matches 14: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

OY 1 KSDPTQETFGALDLGASTQ 19
DB 202 ETNNOETFGALDLGASTQ 220

RESULT 2
S63501
aprase (EC 3.6.1.5) - human (fragments)
N:Alternate names: App diphosphohydrolase
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S63501
R:Christoforidis, S.; Papanarcaki, T.; Galatis, D.; Kellner, R.; Tsolas, O.
Eur. J. Biochem. 224, 66-74, 1995
A:Title: Purification and properties of human placental ATP diphosphohydrolase.
A:Reference number: S63501; MUID:96096723; PMID:8529670
A:Accession: S63501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3:4-8-9-13;14-20;21-30;31-44 <CHR>
C:Keywords: hydrolase

Query Match 64.6% Score 62: DB 2: Length 44:
Best Local Similarity 85.7% Pred. No. 0.001:
Matches 12: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

OY 6 ETYQALDLGASTQ 19
DB 28 DLVQALDLGASTQ 41

RESULT 3

T04439

hypothetical protein T18B16.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04439

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansong, W.; Bancroft, I.; Mewes, H.W.

submitted to the Protein Sequence Database, April 1998

A:Accession: T04439

A:Reference number: 215359

A:Molecule type: DNA

A:Residues: 1-1052 <BEV>

A:Cross-references: EMBL:AL021687

A:Experimental source: cultivar Columbia; BAC clone T18B16

C:Genetics:

A:Map position: 4

A:Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3

A:Note: T18B16.150

Query Match

Best Local Similarity 76.9%; Score 53; DB 2; Length 1052;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 TYGALDLCGASTQ 19

Db 685 TFGALDLCGSLQ 697

RESULT 4

S50463

hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002

C:Accession: S50463

R:Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda

A:Reference number: S50463

A:Accession: S50463

A:Molecule type: DNA

A:Residues: 1-630 <DIE>

A:Cross-references: EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005; MIPS:YER005w

C:Genetics:

A:Gene: SGD:YND1; MIPS:YER005w

A:Cross-references: SCD:S0000807

A:Map position: 5R

Query Match

Best Local Similarity 54.2%; Score 52; DB 2; Length 630;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TYGALDLCGASTQ 19

Db 179 TFGMDMGASTQ 191

RESULT 5

T39109

probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T39109

R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.

submitted to the EMBL Data Library, October 1999

A:Reference number: 221828

A:Accession: T39109

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-556 <BAR>

A:Cross-references: EMBL:AL121741; PID:CA857338.1; GSPDB:GN00066; SPDB:SPAC824.08

A:Experimental source: strain 972h; cosmid c824

C:Genetics:

A:Gene: SPDB:SPAC824.08

A:Map position: 1

Query Match

Best Local Similarity 53.1%; Score 51; DB 2; Length 556;

Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 TQETYGALDLCGASTQ 19

Db 276 THSTVAVMDLCGASTQ 291

RESULT 6

T16696

hypothetical protein R07E4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16696

R:Miller, N.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid R07E4.

A:Reference number: 218561

A:Accession: T16696

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-557 <ML>

A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PID:AAA80403.1; CESP:R0

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:R07E4.4

A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match

Best Local Similarity 52.1%; Score 50; DB 2; Length 557;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETYGALDLCGASTQ 19

Db 212 QKTVMIDMGASAQ 226

RESULT 7

D86276

hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: D86276

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Nelson, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Malt, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MIMD:21016719; PMID:11130712

A:Accession: D86276

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <STO>

A:Cross-references: GB:AE005172; NID:g5080801; PID:AND39311.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match

Best Local Similarity 51.0%; Score 49; DB 2; Length 483;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDTQETYGALDLCGASTQ 19

Db 212 TDPLETGTGIVELGASAQ 229

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:22:16 ; Search time 11 Seconds
(without alignments)

71.641 Million cell updates/sec

Title: US-09-781-796B-7

Perfect score: 96
Sequence: 1 KSPDQETGYGALDLAGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	92	95.8	510	1 ENP1_PIG	Q9MYU4 sus scrofa
2	92	95.8	510	1 ENP1_HOVIN	O18956 bos taurus
3	75	78.1	510	1 ENP1_HUMAN	P49961 homo sapien
4	75	78.1	510	1 ENP1_MOUSE	P55772 mus musculu
5	66	68.8	511	1 ENP1_RAT	P97687 rattus norv
6	65	67.7	469	1 ENP5_MESAU	Q9QUC8 mesocricetu
7	64	66.7	427	1 ENP5_MOUSE	O9WU29 mus musculu
8	64	66.7	428	1 ENP5_HUMAN	O75355 homo sapien
9	62	64.6	529	1 ENP1_HUMAN	O93295 gallus gall
10	58	60.4	493	1 ENP1_CHICK	O9Y513 homo sapien
11	56	58.3	495	1 ENP2_HUMAN	O55026 mus musculu
12	56	58.3	495	1 ENP2_MOUSE	O35795 rattus norv
13	56	58.3	495	1 ENP2_RAT	P79784 gallus gall
14	54	56.2	494	1 ENP2_CHICK	P40009 saccharomyc
15	52	54.2	630	1 YND1_YEAST	Q21815 caenorhabdi
16	50	52.1	552	1 YBU4_CAEEL	Q9E313 rattus norv
17	48	50.0	455	1 ENP6_RAT	O9EBC4 mus musculu
18	48	50.0	613	1 ENP4_MOUSE	P26200 dictyostell
19	47	49.0	124	1 PRO2_DICDI	O9Y227 homo sapien
20	47	49.0	616	1 ENP6_HUMAN	O75354 homo sapien
21	46	47.9	484	1 ENP4_HUMAN	O46894 galliarbia
22	44	45.8	204	1 RK3_GUTTH	Q11026 mycobacteri
23	44	45.8	263	1 YD56_MYCTU	P39353 escherichia
24	44	45.8	372	1 YJHC_ECOLI	P52914 plasmu saliv
25	44	45.8	455	1 NTPA_PEA	P80595 solanum tub
26	41	42.7	454	1 APY_SOLTU	P13682 homo sapien
27	41	42.7	519	1 ZN35_HUMAN	P48601 caenorhabdi
28	40	41.7	439	1 PRS4_DROME	O18411 caenorhabdi
29	40	41.7	485	1 Y14E_CAEEL	P73774 saccharomyc
30	40	41.7	808	1 INFE_ECOLI	P10870 lactococcus
31	40	41.7	818	1 SNF3_YEAST	O9CHU2 lactococcus
32	39	40.6	294	1 M1AA_LACLA	O97TW5 streptococc
33	39	40.6	294	1 M1AA_STRPN	

34	39	40.6	505	1 SPKD_SYNZ3	P54735 synechocyst
35	39	40.6	518	1 GDAI_YEAST	P32621 saccharomyc
36	39	40.6	591	1 DNAK_MYCCA	P45958 mycoplasma
37	39	40.6	1433	1 Y310_HUMAN	O15027 homo sapien
38	38.5	40.1	299	1 M1AA_STRPN	O9A059 streptococc
39	38	39.6	195	1 TRX7_HUMAN	P78412 homo sapien
40	38	39.6	237	1 VD03_VACCC	P21009 vaccinia vl
41	38	39.6	237	1 VD03_VACCV	P04302 vaccinia vl
42	38	39.6	237	1 VD03_VAVR	P33068 variola vlr
43	38	39.6	332	1 AXHA_ASPNG	P79019 aspergillus
44	38	39.6	509	1 SYK_ACICA	O43990 acinetobact
45	38	39.6	587	1 MCB1_AARAT	O91dd8 arabidopsis

ALIGNMENTS

```

RESULT 1
ID      ENP1_PIG      STANDARD:      PRT:      510 AA.
AC      Q9MYU4:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE      (NTPcase1) (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell
DE      activation antigen) (Ecto-ATPase) (CD39 antigen).
GN      ENTPL1 OR CD39
OS      Sus scrofa (Pig).
OC      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Arctic endothelium;
RX      MEDLINE=20325090; PubMed=10866813;
RA      Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benitezak O.,
RA      Sevigny J.,
RT      "Distribution, cloning, and characterization of porcine nucleoside
RT      triphosphate diphosphohydrolase-1."
RL      Eur. J. Biochem. 267:4106-4114(2000).
RN      [2]
RP      SEQUENCE OF 202-220.
RC      TISSUE=Pancreas;
RX      Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA      Beaudoin A.R., Bach F.H., Robson S.C.;
RT      Identification and characterization of CD39/Vascular ATP
RT      diphosphohydrolase.
RL      J. Biol. Chem. 271:33116-33122(1996).
CC      - FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
CC      NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
CC      BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
CC      HYDROLYSES ATP AND ADP EQUALLY WELL.
CC      - CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC      - COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
CC      - SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).
CC      - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC      - TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN VASCULAR
CC      ENDOTHELIUM, SMOOTH MUSCLE, SPLEEN AND LUNG.
CC      - PUT: CLEAVED IN TWO POLYPEPTIDES THAT SEEM TO STAY TOGETHER BY
CC      NONCOVALENT INTERACTIONS.
CC      - SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      EMBL, AJ133746; CAB95871.1;

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DR	InterPro: IPR000407; GDAI_CD39_NTPase.
DR	Pfam: PF01150; GDAI_CD39_1.
DR	PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
KW	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT	CHAIN 1 510
FT	CHAIN 1 201
FT	CHAIN 202 510
FT	DOMAIN 1 16
FT	TRANSMEM 17 37
FT	DOMAIN 38 477
FT	TRANSMEM 478 498
FT	DOMAIN 499 510
FT	CARBOHYD 73 73
FT	CARBOHYD 245 245
FT	CARBOHYD 274 274
FT	CARBOHYD 291 291
FT	CARBOHYD 333 333
FT	CARBOHYD 370 370
FT	CARBOHYD 457 457
FT	CONFLICT 203 203
SQ	SEQUENCE 510 AA; 57757 MW; 82F86869040D735 CRC64;
Query Match	95.8%; Score 92; DB 1; Length 510;
Best Local Similarity	94.7%; Pred. No. 2.5e+06;
Matches 18; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 KSDPNEYGALDLGASSTO 19
Db	202 KGDTQETYGALDLGASSTO 220
RESULT 2	
ID	ENPI_BOVIN STANDARD; PRT: 513 AA.
AC	018956;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell activation antigen) (CD39 antigen) (Ecto-apyrase).
GN	ENTPDI OR CD39.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX	NGBL_Taxid:9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	TISSUE=ortic endocheilium;
RA	Chang A.-S., Garcia R.L., Chang S.M., Schilling W.P.;
RL	Submitted (MAY-1997) to the EMBL/GenBank/DDBB databases.
RL	[2]
RP	SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC	TISSUE=Aorta;
RX	MEDLINE=97115858; PubMed=8955160;
RA	Kaczmarek E., Kozlak K., Seviny J., Siegel J.B., Anrather J.,
RA	Beaudoin A.R., Bach F.H., Robson S.C.;
RT	Identification and characterization of CD39/vascular ATP
RT	diphosphohydrolase.";
J	J. Biol. Chem. 271:33116-33122(1996).
-1-	FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
CC	NUTRIENTS TO REGULATE PRIMERGENIC NEUROTRANSMISSION. COULD ALSO
CC	BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
CC	HYDROLYSES ATP AND ADP EQUALLY WELL.
-1-	CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC	COPROCTOR: REQUIRES CALCIUM AND MAGNESIUM.
-1-	SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1-	SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.

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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF005940; AAB62382.1; -.
DR      Interpro: IPR000407; GDAI.CD39_NTPase.
DR      Pfam: PF01150; GDAI.CD39.1.
DR      ProSITE: PS01238; GDAI.CD39_NTPase.1.
KW      Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT      DOMAIN              1       16
FT      TRANSMEM            17       37
FT      TRANSMEM            38       481
FT      TRANSMEM            482       502
FT      DOMAIN              503       513
FT      CARBOHYD            73       73
FT      CARBOHYD            227       227
FT      CARBOHYD            245       245
FT      CARBOHYD            307       307
FT      CARBOHYD            336       336
FT      CARBOHYD            373       373
FT      CARBOHYD            460       460
FT      CONFLICT            97       97
FT      CONFLICT            101      103
FT      CONFLICT            164       464
SQ      SEQUENCE           513 AA; 58113 MW; 20FE98FE27BD2D96 CRC64;
Oy      1 KSDPTETGALDIDGASTQ 19
Db      202 KDDTETTGALDIDGASTQ 220
RESULT 3
ENP1_HUMAN
ID   ENP1_HUMAN              STANDARD;          PRT;          510 AA.
AC   P49961; G9Y009; Q9Y309;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE   (NTPase) (ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE   activation antigen) (Ecto-apyrase) (CD39 antigen).
GN   ENTPD1 OR CD39.
OS   Homo sapiens (Human).
OC   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID:9606;
RN   [1]
RP      SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RX   MEDLINE=95015846; PubMed=7930580;
RA   Maliszewski C.R., Delespesse G.D.T., Schoenhorn M.A., Armatage R.J.,
RA   Fawcett W.C., Nakajima T., Baker E., Sutherland G.R., Polndexter K.,
RA   Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
RT   "The CD39 Lymphoid cell activation antigen. Molecular cloning and
RT   structural characterization".
J. Immunol. 153:3574-3583(1994).
RN   [2]
RP      SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RX   MEDLINE=97149443; PubMed=8996251;
RA   Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K.,
RA   Millan M., Hancock W.W., Bach F.H.;
RT   "Loss of ATP diphosphohydrolase activity with endothelial cell
RT   activation".
J. Exp. Med. 185:153-163(1997).

```

[3] SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND II).
 RC TISSUE-Placenta:
 RX MEDLINE=99332082; PubMed=10405171;
 RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
 RT Titani K., Fujimura Y., Marita N.;
 "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
 and II.";
 RL FEBS Lett. 453:335-340(1999).
 RN [4]
 RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
 RC TISSUE-Placenta:
 RX MEDLINE=96096723; PubMed=8529670;
 RA Christoforidis S., Papamarcaki T., Galanis D., Kellner R., Tsolas O.;
 RT "Purification and properties of human placental ATP
 diphosphohydrolase.";
 RL Eur. J. Biochem. 234:66-74(1995).
 RN [5]
 RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND
 399-405 (ISOFORM PLACENTAL I).
 RC TISSUE-Placenta:
 RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Marita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.;
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature
 distinct from CD39, localization and inhibition on shear-induced
 platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=97115858; PubMed=8955160;
 RA Kaczmarek E., Kozlak K., Sevianny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC -1- HYDROLYSES ATP AND ADP EQUALLY WELL.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: VASCULAR (SHOWN HERE), PLACENTAL
 I AND PLACENTAL II; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY ON ACTIVATED LYMPHOID
 CELLS. ALSO EXPRESSED IN ENDOTHELIAL TISSUES. THE VASCULAR ISOFORM
 AND THE PLACENTAL ISOFORM II ARE PRESENT IN BOTH PLACENTA AND
 UMBILICAL VEIN, WHEREAS PLACENTAL ISOFORM I IS PRESENT IN PLACENTA
 ONLY.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: OPTIMAL PH IS 7.0-7.5 WITH ATP AS SUBSTRATE AND
 7.5-8.0 WITH ADP.
 CC -1- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD39 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd39.htm"
 CC -----
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 CC -----
 DR EMBL: S73613; AAB32152.1; -;
 DR EMBL: U87967; AAB47572.1; -;
 DR EMBL: AJ131313; CAB41886.1; -;
 DR EMBL: AJ131314; CAB41887.1; -;
 DR GenBank: HGNC:3363; ENTPD1.
 DR MIM: 601752; -;
 DR InterPro: IPR000407; GDAI_CD39_NTPase.

DR Pfam: PF01150; GDAI_CD39.1.
 DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
 KW Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium;
 KM Alternative splicing.
 FT DOMAIN 1 16
 FT TRANSMEM 38 478
 FT DOMAIN 479 499
 FT TRANSMEM 500 510
 FT DOMAIN 73 73
 FT CARBOHYD 227 227
 FT CARBOHYD 292 292
 FT CARBOHYD 334 334
 FT CARBOHYD 371 371
 FT CARBOHYD 457 457
 FT VARSPLIC 1 4
 FT VARSPLIC 272 299
 FT VARSPLIC 300 510
 FT CONFLICT 57 58
 FT CONFLICT 162 162
 FT CONFLICT 208 208
 FT CONFLICT 248 248
 FT CONFLICT 510 AA; 57964 MW; BAD87D2499649159 CRC64;
 SO SEQUENCE
 Query Match 78.1%; Score 75; DB 1; Length 510;
 Best Local Similarity 73.7%; Pred. No. 2.3e-05;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSDQETGYGALDLGGASTO 19
 DB 202 ETNNQETFGALDLGGASTO 220
 RESULT 4
 ENTPD_MOUSE STANDARD; PRT; 510 AA.
 ID ENTPD_MOUSE
 AC P55772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (Ntpdase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
 DE activating antigen) (Ecto-apyrase) (CD39 antigen).
 GN ENTPD1 OR CD39.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95015846; PubMed=7930580;
 RA Maliszewski C.R., Delaspese G.J.T., Schoenborn M.A., Armistead R.J.,
 RA Fawcett W.C., Nakajima Y., Baker E., Sutherland G.R., Polidexter K.,
 RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
 RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
 RT structural characterization.";
 RL J. Immunol. 153:3574-3583(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SyJ;
 RX MEDLINE=96399871; PubMed=9730622;
 RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
 RA Gayle R.B. III, Maliszewski C.R.;
 RT "Gene structure and chromosome location of mouse Cd39 coding for an
 RT ecto-apyrase.";
 RL Cytogenet. Cell Genet. 81:287-289(1998).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND ADP EQUALLY WELL.

SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN-Sprague-Dawley: TISSUE-brain, and Hippocampus;
MEDLINE-96215267: Pubmed-8626624;
Mang T.-F., Rosenberg P.A., Guldotti G.;
"Characterization of brain ecto-ATPase: evidence for only one ecto-
ATPase (CD9) gene.";
Brain Res. Mol. Brain Res. 47:295-302(1997).
[2]

Accession	Strain	PKI	409 AA.
C09QYC8; Q9QYC9;	GRINDAD,		
16-OCT-2001 (Rel. 40, Created)			
16-OCT-2001 (Rel. 40, Last sequence update)			

DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 DE (EC 3.6.1.6) (NTPases5) (Nucleoside diphosphatase) (CD39 antigen-like
 DE 4) (ER-UDPase) (Proto-oncogene cph).
 GN ENTPD5 OR CD39L4 OR CPH.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99142925; PubMed=9989819;
 RA Velasco J.A., Avila M.A., Notario V.;
 RT "The product of the cph oncogene is a truncated, nucleotide-binding
 RT protein that enhances cellular survival to stress-";
 RL Oncogene 18:689-701(1999).
 CC -1- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYRIPHOSPHATE
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT
 CC TISSUES.
 CC -1- DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC
 CC POTENTIAL.
 CC -1- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: AF084568; AAF2931.1; ALT_TERM.
 CC DR EMBL: AF084568; AAF2932.1; -
 CC DR InterPro: IPR000407; GDAI-CD39_NTPase.
 CC DR Pfam: PF01150; GDAI-CD39_1.
 CC DR PROSITE: PS01238; GDAI-CD39_NTPASE; FALSE_NEG.
 CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Endoplasmic reticulum; Signal; Proto-oncogene.
 CC FT SIGNAL 1 18 POTENTIAL.
 CC FT CHAIN 19 469 ECTONUCLEOSIDE TRIPHOSPHATE
 CC FT CARBOHYD 42 42 DIPHOSPHOHYDROLASE 5.
 CC FT CARBOHYD 232 232 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT SEQUENCE 469 AA; 52125 MW; 03DBA23E0C73474B CRC64;
 CC SQ
 CC Query Match 67.7%; Score 65; DB 1; Length 469;
 CC Best Local Similarity 81.2%; Pred. No. 0.0012; Indels 0; Gaps 0;
 CC Matches 13; Conservative 1; Mismatches 2;
 CC
 CC QY 4 TOERTYALDGGASTQ 19
 CC :||| |||||
 CC DB 191 SQETWGTLDGASTQ 206
 CC
 CC RESULT 7
 CC ID ENPS_MOUSE STANDARD: PRT; 427 AA.
 CC AC 09WU29: 070214;
 CC DT 16-OCT-2001 (Rel. 40; Created)
 CC DT 16-OCT-2001 (Rel. 40; Last sequence update)
 CC DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 CC DE (EC 3.6.1.6) (NTPases5) (Nucleoside diphosphatase) (CD39 antigen-like
 CC DE 4) (ER-UDPase).
 CC GN ENTPD5 OR CD39L4.

OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Testis;
 RX MEDLINE=98119025; PubMed=9457681;
 RT Chadwick B.P., Williamson J., Sheer D., Frischaut A.-M.;
 RT "cDNA cloning and chromosomal mapping of a mouse gene with homology to
 RT NTPases-";
 RL Mamm. Genome 9:162-164(1998).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
 RC TISSUE-Liver;
 RX MEDLINE=99298181; PubMed=10369669;
 RA Trombetta E.S., Helenius A.;
 RT "Glycoprotein reglycosylation and nucleotide sugar utilization in the
 RT secretory pathway: identification of a nucleoside diphosphatase in the
 RT endoplasmic reticulum-";
 RL EMBO J. 18:3282-3292(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Akawa T., Hara A., Fukunishi Y., Komori H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl L., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshyn-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection-";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE
 CC PYRIPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- TISSUE SPECIFICITY: UNIDIRECTIONAL.
 CC -1- PTM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCANS.
 CC -1- MISCELLANEOUS: OPTIMAL pH IS NEUTRAL.
 CC -1- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC DR EMBL: AF006482; AAC05181.1; -
 CC DR EMBL: AJ238636; CAB45533.1; -
 CC DR EMBL: AK002618; BAB22234.1; -
 CC DR MGD: MGI:1321385; ENTPD5.
 CC DR InterPro: IPR000407; GDAI-CD39_NTPase.
 CC DR Pfam: PF01150; GDAI-CD39_1.

DW	PROSITE: PS01238; GDAI-CD39_NTPASE; FALSE_NEG.
KR	Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW	Endoplasmic Reticulum; Signal.
FT	SIGNAL
FT	CHAIN
FT	POTENTIAL.
FT	ECTONUCLEOSIDE TRIPHOSPHATE
FT	DIPHOSPHOHYDROLASE 5.
FT	N-LINKED (GICNNC . . .) (POTENTIAL).
FT	CARBOHYD 232 232 N-LINKED (GICNNC . . .) (POTENTIAL).
FT	CARBOHYD 368 368 N-LINKED (GICNNC . . .) (POTENTIAL).
SO	SEQUENCE 428 AA; 47517 MW; 830437A15D64DDD CRC04;
Query Match	
Best Local Similarity 66.7%;	
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	Score 64; DB 1; Length 428;
Ped. No. 0.0016;	
DB 192 OETVGLDIGASTQ 206	
5 OETYGALDIGASTQ 19	

RESULT# 9			
ID	ENP3_HUMAN	STANDARD:	PRT: 529 AA.
AC	073355; 060495;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	Econucleoside triphosphate diphosphotriolase 3		
DE	(NTPDase) (Ecto-ATP diphosphotriolase) (ATPase) (Ecto-ATPase)		
DE	(CD39 antigen-like 3) (hdb).		
GN	ENPD3 OR CD39L3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
PN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Keratinocytes;		
RX	MEDLINE=98341119; PubMed=9676430;		
RA	Chadwick B.P., Fritschau A.-M.;		
RT	"The CD39-like gene family: identification of three new human members		
RT	(CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of		
RL	the gene family from Drosophila melanogaster.";		
RL	Genomics 50:357-367(1998).		
UN	[2]		
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.		
RC	TISSUE=Brain;		
RX	MEDLINE=98342144; PubMed=9675246;		
RA	Smith T.M., Kirley T.L.;		
RT	"Cloning, sequencing, and expression of a human brain ecto-ATPase		
RT	related to both the ecto-ATPases and CD39 ecto-ATPases.";		
RL	Biochem. Biophys. Acta 1386:65-78(1998).		
RP	[3]		
UN	REVISIONS.		
RA	Smith T.M., Kirley T.L.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
UN	[4]		
RP	MUTAGENESIS OF TRP-187, ASP-219 AND TRP-459.		
RX	MEDLINE=99249795; PubMed=1021336;		
RA	Smith T.M., Lewis Carl S.A., Kirley T.L.;		
RT	"Mutagenesis of two conserved tryptophan residues of the E-type		
RT	ATPases: Inactivation and conversion of an ecto-ATPase to an		
RT	ecto-NTPase.";		
RL	Biochemistry 38:5849-5857(1999).		
UN	[5]		
RP	MUTAGENESIS OF R-67; R-143; R-146; E-182; N-191; S-224 AND Q-226.		
RX	MEDLINE=21197753; PubMed=1100774;		
RA	Yang P., Hicks-Berger C.A., Smith T.M., Kirley T.L.;		
RT	"Site-directed mutagenesis of human nucleoside triphosphate		
RT	diphosphotriolase 3: the importance of residues in the ATPase		
RT	conserved regions.";		
RL	Biochemistry 40:3943-3950(2001).		

CC ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND A
 CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- INDUCTION: BY DIOXIN.
 CC -1- PIM: HAS PROBABLY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: U91511; AAB81014.1; -;
 CC EMBL: AF042811; AAC24347.1; -;
 CC EMBL: AK002553; BAB22182.1; -;
 CC MGD: MGI1096863; Entrez: -;
 CC DR InterPro: IPR000407; GDAI_CD39_NTPase.
 CC DR Pfam: PF01150; GDAI_CD39.1.
 CC DR PROSITE: PS01238; GDAI_CD39_NTPase.1.
 CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Alternative splicing.
 CC FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 5 25 POTENTIAL.
 CC FT DOMAIN 26 462 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 463 483 POTENTIAL.
 CC FT DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 130 132 LTS -> MAG (IN SHORT ISOFORM).
 CC FT VARSPPLIC 133 495 MISSING (IN SHORT ISOFORM).
 CC FT VARSPPLIC 400 400 T -> A (IN REF. 3).
 CC FT CONFLICT 414 414 S -> R (IN REF. 3).
 CC FT CONFLICT 437 437 T -> A (IN REF. 3).
 CC FT CONFLICT 437 437 T -> R (IN REF. 3).
 CC SQ SEQUENCE 495 AA; 54310 MW; CC0811C5D79CA48 CRC64;
 CC -----
 CC Query Match 58.3%; Score 56; DB 1; Length 495;
 CC Best Local Similarity 84.6%; Pred. No. 0.046;
 CC Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC OY 7 TYGALDLGGASTQ 19
 CC Db 196 TLGAMDLGGASTQ 208
 CC -----
 CC RESULT 13
 CC ENP2_RAT STANDARD; PRT: 495 AA.
 CC AC 035795; 090H5; 09WVE;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
 CC DE (NTPase2) (Ecto-ATPase) (CD39 antigen-like 1).
 CC DE ENTPD2 OR CD39L1.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_Taxid:10116;
 CC [1]
 CC RM SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 CC RP STRAIN-Sprague-Dawley; TISSUE-Brain;
 CC RX MEDLINE:98031057; PubMed:9354474;
 CC RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;

RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 RT rat brain.";
 RT RL Neuropharmacology 36:1189-1200(1997).
 RT [2]
 RT RP SEQUENCE FROM N.A. (ISOFORM 1).
 RT RC STRAIN-Sprague-Dawley; TISSUE-Sertoli cells;
 RT RX MEDLINE:21121474; PubMed:11229804;
 RT RA Lu O., Porter L.D., Cui X., Sanborn B.M.;
 RT "Ecto-ATPase mRNA is regulated by FSH in Sertoli cells.";
 RT J. Androl. 22:289-301(2001).
 RT [3]
 RT RP SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2).
 RT RC STRAIN-Wistar; TISSUE-Cochlea;
 RT RX MEDLINE:20050856; PubMed:10581401;
 RT RA Vlahkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 RT termination of purinergic transmission.";
 RT Brain Res. Mol. Brain Res. 73:85-92(1999).
 RT RL Brain Res. 73:85-92(1999).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES
 CC ADP ONLY TO A MARGINAL EXTENT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS,
 CC KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION
 CC IN LIVER.
 CC -1- INDUCTION: BY FSH IN SERTOLI CELLS BUT NOT IN PERITUBULAR CELLS;
 CC BY CAMP IN BOTH TYPE OF CELLS.
 CC -1- PIM: HAS PROBABLY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y11835; GAA72533.1; -;
 CC EMBL: AF276940; AAB87740.1; -;
 CC EMBL: AF129103; AAD42303.1; -;
 CC DR InterPro: IPR000407; GDAI_CD39_NTPase.
 CC DR Pfam: PF01150; GDAI_CD39.1.
 CC DR PROSITE: PS01238; GDAI_CD39_NTPase.1.
 CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Alternative splicing.
 CC FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 5 25 POTENTIAL.
 CC FT DOMAIN 26 462 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 463 483 POTENTIAL.
 CC FT DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 130 132 LTS -> MAG (IN SHORT ISOFORM).
 CC FT VARSPPLIC 133 495 MISSING (IN SHORT ISOFORM).
 CC FT VARSPPLIC 400 400 T -> A (IN REF. 2).
 CC FT CONFLICT 127 128 PF -> L (IN REF. 2).
 CC FT CONFLICT 339 339 L -> T (IN REF. 2).
 CC FT CONFLICT 444 444 L -> F (IN REF. 2).
 CC SQ SEQUENCE 495 AA; 54389 MW; 237B999F1BBE8E00 CRC64;
 CC -----
 CC Query Match 58.3%; Score 56; DB 1; Length 495;
 CC Best Local Similarity 84.6%; Pred. No. 0.046;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 7 TYGALDLCGASTQ 19
 Db 196 TLGAMDLGGASTQ 208

RESULT 14
 ENP2_CHICK
 ID ENP2_CHICK STANDARD; PRT; 494 AA.
 AC P79784;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
 DE (NTPase2) (ecto-ATPase) (CD39 antigen-like 1).
 GN ENTPD2 OR CD39L1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21, 68-73; 83-90; 108; 121;
 RP 144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380;
 RP 383-389; 448-456 AND 459-479.
 RC TISSUE-Skeletal muscle, and Gizzard;
 RX MEDLINE=97150869; PubMed=8995405;
 RX Kirley T.L.;
 RT "Complementary DNA cloning and sequencing of the chicken muscle ecto-
 RT ATPase. Homology with the lymphoid cell activation antigen CD39.";
 RL J. Biol. Chem. 272:1076-1081(1997).
 RN [2]
 RP SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION.
 RX MEDLINE=95081479; PubMed=7989647;
 RX Stout J.G., Kirley T.L.;
 RT "Purification and characterization of the ecto-Mg-ATPase of chicken
 RT gizzard smooth muscle.";
 RL J. Biochem. Biophys. Methods 29:61-75(1994).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE FURTHER NEUROTANSMISSION. HYDROLYZES
 CC ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- PTM: HAS PROBABLY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U74467; AAC60071.1;
 DR InterPro: IPR000407; GDAL_CD39_NTPase.
 DR Pfam: PF01150; GDAL_CD39.1.
 DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 DR Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium.
 KM Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium.
 FT INT_MET 0
 FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 4 24 POTENTIAL.
 FT DOMAIN 25 464 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 465 485 POTENTIAL.
 FT DOMAIN 486 494 POTENTIAL.
 FT TRANSSEM 495 517 POTENTIAL.
 FT CARBOHYD 61 13 POLY-LEU.
 FT CARBOHYD 296 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 11 11 L -> LL (IN REF. 2).

FT CONFLICT 174 176 ENF -> GNK (IN REF. 2).
 SQ SEQUENCE 494 AA; 54402 MW; 1E0DE631DA621EE CRC64;
 Query Match 56.2%; Score 54; DB 1; Length 494;
 Best Local Similarity 66.7%; Pred. No. 0.1;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 5 QETGALDLCGASTQ 19
 Db 190 KKTGLAMDLGGASTQ 204
 RESULT 15
 YND1_YEAST
 ID YND1_YEAST STANDARD; PRT; 630 AA.
 AC P40009;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (adenosine
 DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
 DE diphosphatase).
 GN YND1 OR YER005W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 RA Aviles E., Bero A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkle-Smith S.,
 RA Hyman R., Kayser A., Komp C., Laskari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
 RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
 RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
 RL submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=S288c;
 RX MEDLINE=99340091; PubMed=10409709;
 RX Gao X.D., Katsorodov V., Jigam Y.;
 RT "YND1, a homologue of GDAL, encodes membrane-bound apyrase required
 RT for Golgi N- and O-glycosylation in Saccharomyces cerevisiae.";
 RL J. Biol. Chem. 274:21450-21456(1999).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF PHOSPHOANHYDRIDE BONDS OF
 CC NUCLEOSIDE TRI- AND DI-PHOSPHATES. HAS EQUAL HIGH ACTIVITY TOWARD
 CC ADP/ATP, GDP/GTP, AND UDP/UTP AND APPROXIMATELY 50% LESS TOWARD
 CC GMP/CTP AND THIAMINE PYROPHOSPHATE. HAS NO ACTIVITY TOWARD GMP.
 CC REQUIRED FOR GOLGI GLYCOSYLATION AND CELL WALL INTEGRITY.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -1- PATHWAY: Glycosylation.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND; GOLGI.
 CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
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 CC -----
 DR EMBL: U18778; AAB64538.1;
 DR EMBL: AF203695; AAP17573.1;
 DR SGD: S0000807; YND1.
 DR InterPro: IPR000407; GDAL_CD39_NTPase.
 DR Pfam: PF01150; GDAL_CD39.1.
 DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 DR Hydrolase; Transmembrane; Golgi stack.
 KM Domain 1 500 LUMENAL (POTENTIAL).
 FT TRANSSEM 501 517 POTENTIAL.

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:33:31 ; Search time 92 Seconds
(without alignments)
42.553 Million cell updates/sec

Title: US-09-781-796B-7
Perfect score: 96
Sequence: 1 KSDQETFGALDGGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	78.1	510	11 092106	092106 mus musculu
2	64	66.7	407	4 08MUB3	08MUB3 homo sapien
3	64	66.7	428	4 096RX0	096RX0 homo sapien
4	58	60.4	493	13 090X66	090X66 gallus gall
5	58	60.4	681	10 085613	085613 oryza sativ
6	56	58.3	495	11 0921R1	0921R1 mus musculu
7	54	56.2	300	11 09D813	09D813 mus musculu
8	53	55.2	1052	10 049676	049676 arabidopsis
9	51	53.1	556	3 09RT35	09RT35 schizosach
10	49	51.0	483	3 09RT62	09RT62 arabidopsis
11	48	50.0	447	10 09RT11	09RT11 pismu sativ
12	48	50.0	448	11 08R001	08R001 mus musculu
13	48	50.0	462	10 09XFC9	09XFC9 dolichos bl
14	48	50.0	635	10 08S7E1	08S7E1 oryza sativ
15	47	49.0	467	10 08RV76	08RV76 pismu sativ
16	47	49.0	606	11 09ET10	09ET10 mus musculu

17	47	49.0	690	5 09BRV5	09BRV5 leishmania
18	46.5	48.4	572	3 09USP2	09USP2 schizosach
19	46.5	48.4	604	4 09N027	09N027 homo sapien
20	46	47.9	148	10 09XGR6	09XGR6 xanthoceras
21	46	47.9	483	4 08RTA7	08RTA7 homo sapien
22	46	47.9	550	4 09NTN2	09NTN2 homo sapien
23	45	46.9	476	2 09R011	09R011 bacteroides
24	44.5	46.4	326	10 09AUI4	09AUI4 medicago tr
25	44	45.8	405	10 09M9T7	09M9T7 arabidopsis
26	44	45.8	407	10 09AVN8	09AVN8 pismu sativ
27	44	45.8	447	10 09SLV4	09SLV4 pismu sativ
28	44	45.8	455	10 09FEA6	09FEA6 pismu sativ
29	44	45.8	455	10 08RVU0	08RVU0 pismu sativ
30	44	45.8	461	5 08RTY9	08RTY9 pismu sativ
31	44	45.8	461	5 076268	076268 drosophila
32	44	45.8	464	5 09V018	09V018 drosophila
33	44	45.8	471	10 09S0G2	09S0G2 arabidopsis
34	44	45.8	472	10 09M7B3	09M7B3 arabidopsis
35	44	45.8	472	10 09SPM5	09SPM5 arabidopsis
36	44	45.8	473	10 08RTM8	08RTM8 pismu sativ
37	44	45.8	555	10 094E22	094E22 arabidopsis
38	44	45.8	555	10 080612	080612 arabidopsis
39	44	45.8	925	12 069138	069138 human herpe
40	44	45.8	2139	3 09P880	09P880 botrytis ci
41	44	45.8	2225	5 09VJ82	09VJ82 drosophila
42	43	44.8	313	16 09P206	09P206 streptomyces
43	43	44.8	456	10 09SPM8	09SPM8 lotus japon
44	43	44.8	468	10 09EVC2	09EVC2 glycine soj
45	43	44.8	494	16 09RB68	09RB68 chlamydia p

ALIGNMENTS

RESULT 1
ID 092106 PRELIMINARY: PRT: 510 AA.
AC 092106;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to ectonucleoside triphosphate diphosphohydrolase 1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; RC011278; A011278.1;
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39_1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 78.1%; Score 75; DB 11; Length 510;
Best Local Similarity 83.3%; Pred. No. 0.00028;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SDRQETFGALDGGASTQ 19
DB 202 SDRQETFGALDGGASTQ 219

RESULT 2
ID 08MUB3 PRELIMINARY: PRT: 407 AA.
AC 08MUB3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to ectonucleoside triphosphate diphosphohydrolase 5.
 OS Homo sapiens (Human)
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleia; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC020966; AAH20966.1; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 KM Hydrolase.
 SQ SEQUENCE 407 AA; 45336 MW; D92A5F7DC9EC9E5B CRC64;
 Query Match 66.7%; Score 64; DB 4; Length 407;
 Best Local Similarity 86.7%; Pred. No. 0.016;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDLCGASTQ 19
 DB 192 QETVGTLDLCGASTQ 206
 RESULT 3
 O96RX0 PRELIMINARY; PRT; 428 AA.
 AC O96RX0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE PcpH proto-oncogene protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleia; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20173601; PubMed=10708485;
 RA Recto J.A., Zambirano N., Pena, Id, Reig J.A., Rhoads A., Rouzaud A.,
 RA Notario V.;
 RT "The human PCPH proto-oncogene: cDNA identification, primary
 RT structure, chromosomal mapping, and expression in normal and tumor
 RT cells";
 RL Mol. Cell. Oncolog. 27:229-236(2000).
 DR EMBL: AF136572; AAK82950.1; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 SQ SEQUENCE 428 AA; 47431 MW; F2C4F7DE650A44P6 CRC64;

Query Match 66.7%; Score 64; DB 4; Length 428;
 Best Local Similarity 86.7%; Pred. No. 0.018;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 QETYGALDLCGASTQ 19
 DB 192 QETVGTLDLCGASTQ 206
 RESULT 4
 O90X66 PRELIMINARY; PRT; 493 AA.
 AC O90X66;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Eco-ATP-diphosphohydrolase (EC 3.6.1.5).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
 RT "Purification, molecular cloning, and expression of the chicken liver
 RT ecto-ATP-diphosphohydrolase";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF426405; AAL25086.1; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR PROSITE: PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.
 KM Hydrolase.
 SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;
 Query Match 60.4%; Score 58; DB 13; Length 493;
 Best Local Similarity 85.7%; Pred. No. 0.22;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ETYGALDLCGASTQ 19
 DB 197 EYLGALDLCGASTQ 210
 RESULT 5
 O8S613 PRELIMINARY; PRT; 681 AA.
 AC O8S613;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative nucleoside phosphatase.
 GN OSJNB0023M1.10.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIPONBARE;
 RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
 RA Kuit K., Nasclmento L., Baker J., Santos L., Zutavern T., Miller B.,
 RA Cummins D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R.,
 RA King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
 RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
 RT OSJNB0023M11, from chromosome 10, complete sequence";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC092749; AAM08556.1; -
 SQ SEQUENCE 681 AA; 75002 MW; B1B8747920580BD CRC64;

Query Match 60.4%; Score 58; DB 10; Length 681;
 Best Local Similarity 61.1%; Pred. No. 0.32;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 SDQETYGALDLCGASTQ 19
 DB 260 SSKMTYGSIDLGGSSLQ 277
 RESULT 6
 Q921R1 PRELIMINARY; PRT; 495 AA.
 AC Q921R1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 2.
 GN ENTPD2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleia; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011241; AAI11241.1; -.
DR MGD: MGI:1096863; Entrez.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39_1.
DR PROSITE: PS01238; GDA1_CD39_NTPase; UNKNOWN_1.
KM Hydrolyase.
SQ SEQUENCE 495 AA; 54319 MW; A76468A0CBF66AAC CRC64;

Query Match 58.3%; Score 56; DB 11; Length 495;
Best Local Similarity 84.6%; Pred. No. 0.49;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TYGALDLAGASTQ 19
Db 196 TLGADLGGASTQ 208

RESULT 7
ID Q9D813 PRELIMINARY; PRT; 300 AA.
AC Q9D813;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 2010320H07RIK protein.
DE 2010320H07RIK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RA MEDLINE=21085560; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa A., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Welz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK008590; BAB25764.1; -.
DR MGD: MGI:1919340; 2010320H07RIK.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39_1.
DR SQUENCE 300 AA; 33646 MW; CCDE372AF12C6B16 CRC64;

Query Match 56.2%; Score 54; DB 11; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GADLGGASTQ 19
Db 4 GADLGGASTQ 14

RESULT 8

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O49676
ID O49676 PRELIMINARY; PRT; 1052 AA.
AC O49676;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical 116.4 kDa protein.
DE T18B16.150 OR A74G19180.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbiales; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Bancroft I.,
RA Mewes H.W., Mayer K., Schueller C.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL021687; CA16707.1; -.
DR EMBL: AL161550; CAB78920.1; -.
DR InterPro: IPR000620; DUF6.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF00892; DUF6; 1.
DR Pfam: PF01150; GDA1_CD39_1.
KM Hypothetical protein.
SQ SEQUENCE 1052 AA; 116388 MW; 88CAFF1F16225987 CRC64;

Query Match 55.2%; Score 53; DB 10; Length 1052;
Best Local Similarity 76.9%; Pred. No. 3.9;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TYGALDLAGASTQ 19
Db 685 TLGADLGGASTQ 697

RESULT 9
ID Q9UT35 PRELIMINARY; PRT; 556 AA.
AC Q9UT35;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative guanosine-diphosphatase (guanosine diphosphatase).
DE SPAC824.08 OR GDP1.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC SFRAIN=972H-;
RA Barrall B.G., Rajandream M.A., Quail M., Seegar K., Harris D.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Sanchez R., Franco A., Notario V., Gacto M., Cansado J.;
RT "Characterization of a guanosine diphosphatase gene from
RT Schizosaccharomyces pombe.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL121741; CAB57338.1; -.
DR EMBL: AF465240; AAI69974.1; -.
DR InterPro: IPR000407; GDA1_CD39_NTPase.

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DR Pfam: PF01150; GDA1_CD39_1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase; 1.
 SO SEQUENCE 556 AA; 61588 MW; 1D811E3D66BB85 CRC64;
 Query Match 53.1%; Score 51; DB 3; Length 556;
 Best Local Similarity 62.5%; Pred. No. 4;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 4 TQETRYGALDYGASTQ 19
 I : : : : :
 DB 276 THSYVAVMDLGGASTQ 291

RESULT 10
 Q9X162 PRELIMINARY; PRT; 483 AA.
 AC Q9X162;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DE F7A19.34 protein.
 GN F7A19.34.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altai H., Araujo R., Hultar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremetska I., Kim C., Ienz C., Li J., Liu S.,
 RA Lutos S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007576; AAD39311.1;
 DR InterPro: IPR00407; GDA1_CD39_NTPase.
 DR InterPro: IPR001092; HLH_Basic.
 DR Pfam: PF01150; GDA1_CD39_1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase; UNKNOWN 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN 1.
 SQ SEQUENCE 483 AA; 53425 MW; 4E31D13830FC8F9 CRC64;
 Query Match 51.0%; Score 49; DB 10; Length 483;
 Best Local Similarity 55.6%; Pred. No. 7.4;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 2 SDTQETRYGALDYGASTQ 19
 : : : : :
 DB 212 TDPLETTGIVELGASAQ 229

RESULT 11
 Q9FU11 PRELIMINARY; PRT; 447 AA.
 AC Q9FU11;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Aprase 2.
 GN APY2.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Jin L., Roux S.J.;
 RA "Cloning of a second Aprase in Pisum sativum";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF305783; AAG22044.1; -

DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39_1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase; 1.
 SO SEQUENCE 447 AA; 48783 MW; 5CB2B0CC7A7F860E CRC64;
 Query Match 50.0%; Score 48; DB 10; Length 447;
 Best Local Similarity 52.9%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 3 DTQETRYGALDYGASTQ 19
 I : : : : :
 DB 187 DYSPTGVVDLGGGSVQ 203

RESULT 12
 Q8R0U1 PRELIMINARY; PRT; 448 AA.
 AC Q8R0U1;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to lysosomal apyrase-like 1 (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Soturognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026420; AAH26420.1; -
 ET NON_TER 1
 SQ SEQUENCE 448 AA; 51285 MW; 0DA6F8BA734E3D6 CRC64;

Query Match 50.0%; Score 48; DB 11; Length 448;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QETRYGALDYGASTQ 19
 : : : : :
 DB 107 KRTAGVLDMGVSTQ 121

RESULT 13
 Q9XFC9 PRELIMINARY; PRT; 462 AA.
 AC Q9XFC9;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Nod factor binding lectin-nucleotide phosphohydrolase.
 GN LNP.
 OS Dolichos biflorus (Horse gram).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.
 OX NCBI_TaxID=3840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ROOT;
 RX MEDLINE=99254131; PubMed=10318974;
 RA Frazier M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
 RA Murphy J.B.;
 RT "A nod factor binding lectin with apyrase activity from legume roots";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).
 DR EMBL: AF139807; AAD31285.1; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39_1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase; 1.
 KW Hydrolase; Lectin.
 SQ SEQUENCE 462 AA; 51183 MW; 59F865A9D4CC444B CRC64;

